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OM protein - protein search, using sw model

Run on: July 21, 2004, 09:59:59 ; Search time 13 Seconds  
(without alignments)  
640.863 Million cell updates/sec

Title: US-10-031-607-7  
Perfect score: 913  
Sequence: 1 MYRLPQVLMGCLLTAVHP.....WLCNRQATRLMLSVPRIG 160

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	795	86.0	277	1_TNR5_HUMAN	P25942 homo sapien
2	558	61.1	269	1_TNR5_BOVIN	Q28203 bos taurus
3	483	52.9	289	1_TNR5_MOUSE	P27512 mus musculus
4	262	28.7	625	1_TR11_MOUSE	Q35305 mus musculus
5	259	28.4	616	1_TR11_HUMAN	Q9Y6G6 homo sapien
6	212.5	23.3	461	1_TR1B_HUMAN	P20333 homo sapien
7	202	22.1	283	1_TR1A_HUMAN	Q92956 homo sapien
8	200	21.9	435	1_TNR3_HUMAN	P36941 homo sapien
9	188.5	20.6	324	1_TNR6_RAT	P36199 rattus norv
10	181	19.8	401	1_T11B_RAT	O08727 rattus norv
11	180	19.7	327	1_TNR6_MOUSE	P25446 mus musculus
12	177	19.4	401	1_T11B_HUMAN	O00300 homo sapien
13	175	19.2	401	1_T11B_MOUSE	O08712 mus musculus
14	173	18.9	474	1_T11B_MOUSE	P25119 mus musculus
15	170	18.6	349	1_CRMB_VARV	P34015 variola vir
16	169	18.5	323	1_TNR6_BOVIN	P51867 bos taurus
17	168	18.4	349	1_CRMB_CAMPS	Q8UYA7 camelpox vi
18	165	18.1	332	1_TNR6_PIG	O77736 sus scrofa
19	165	18.1	335	1_TNR6_HUMAN	P25445 homo sapien
20	164	18.0	204	1_TR26_MOUSE	P83626 mus musculus
21	163	17.9	351	1_CRMB_COMX	O73559 cowpox viru
22	162.5	17.8	280	1_TNR7_HUMAN	P26842 homo sapien
23	153	16.8	415	1_TNR3_MOUSE	P50284 mus musculus
24	151	16.5	250	1_TNR7_MOUSE	P41272 mus musculus
25	145	15.9	271	1_TNR4_RAT	P15725 rattus norv
26	142	15.6	272	1_TNR4_MOUSE	P47741 mus musculus
27	135.5	14.8	277	1_TNR4_HUMAN	P43489 homo sapien
28	130	14.2	416	1_T116_CHICK	P18519 gallus gall
29	129.5	14.2	461	1_TR1A_RAT	P22334 rattus norv
30	129	14.1	326	1_VT2_MYXVL	P29825 myxoma viru
31	128.5	14.1	454	1_TR1A_MOUSE	P25118 mus musculus
32	125.5	13.7	455	1_TR1A_HUMAN	P19438 homo sapien
33	125	13.7	417	1_TR25_HUMAN	Q93038 h tumor nec

34	124	13.6	830	1_SREC_HUMAN	Q14162 homo sapien
35	122	13.4	300	1_TR6B_HUMAN	Q95407 homo sapien
36	116	12.7	325	1_VT2_SFVKA	P25943 Shope fibro
37	115.5	12.7	427	1_TR16_HUMAN	P08138 homo sapien
38	114.5	12.5	417	1_TR16_MOUSE	Q920W1 mus musculus
39	110	12.0	514	1_EDAR_ORYLA	Q90VY2 oryzias lat
40	109.5	12.0	461	1_TR1A_PIG	P50555 sus scrofa
41	108.5	11.9	425	1_TR16_RAT	P07174 rattus norv
42	107	11.7	833	1_DL_DROME	P10041 drosophila
43	107	11.7	1790	1_LMB1_DROME	P11046 drosophila
44	106	11.6	1587	1_LMG3_HUMAN	Q9Y6N6 homo sapien
45	105	11.5	471	1_TR1A_BOVIN	O19131 bos taurus

ALIGNMENTS

RESULT 1  
TNR5\_HUMAN  
ID TNR5\_HUMAN STANDARD; PRT; 277 AA.  
AC P25942; Q9BYU0;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DE Tumor necrosis factor receptor superfamily member 5 precursor  
DE (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).  
GN TNFRSF5 OR CD40.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=89356608; PubMed=2475341;  
RA Stamenkovic I., Clark E.A., Seed B.;  
RT "A B-lymphocyte activation molecule related to the nerve growth  
RT factor receptor and induced by cytokines in carcinomas.";  
RL EMBL J. 8:1403-1410(1989).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM I).  
RX MEDLINE=21638749; PubMed=11780052;  
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaesalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConachie I.J., McIlroy K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.,  
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RT Rogers J.;  
RL "The DNA sequence and comparative analysis of human chromosome 20.";  
RN Nature 414:865-871(2001).  
RP SEQUENCE FROM N.A. (ISOFORM II).  
RX MEDLINE=21117110; PubMed=11172023;  
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;  
RT "Regulation of CD40 function by its isoforms generated through

RT alternative splicing.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM I).  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Straubeberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McKeown F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP INTERACTION WITH TRAF3.  
 RX MEDLINE=95184010; PubMed=7533327;  
 RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;  
 RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";  
 RL Science 267:1494-1498(1995).  
 RN [6]  
 RP INTERACTION WITH TRAF3.  
 RX MEDLINE=9512692; PubMed=7530216;  
 RA Sato I., Irie S., Reed J.C.;  
 RT "A novel member of the TRAF family of putative signal transducing  
 RT proteins binds to the cytosolic domain of CD40.";  
 RL FEBS Lett. 358:113-118(1995).  
 RN [7]  
 RP INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.  
 RX MEDLINE=98384149; PubMed=9718306;  
 RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,  
 RA Kenry M.R.;  
 RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)  
 RT interactions: regulation of CD40 signaling through multiple TRAF  
 RT binding sites and TRAF hetero-oligomerization.";  
 RL Biochemistry 37:11836-11845(1998).  
 RN [8]  
 RP INTERACTION WITH TRAF5.  
 RX MEDLINE=98172745; PubMed=9511754;  
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Hirai M.,  
 RA Otsuka M., Yamamoto T., Inoue J.-I.;  
 RT "Cloning and characterization of a cDNA encoding the human homolog of  
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
 RL Gene 207:135-140(1998).  
 RN [9]  
 RP INTERACTION WITH TRAF6.  
 RX MEDLINE=98095703; PubMed=9432981;  
 RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,  
 RA Okumura K., Yamamoto T., Nagaoaka H., Takemori T.;  
 RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates  
 RT extracellular signal-regulated kinase (ERK) activity in CD40  
 RT signaling along a ras-independent pathway.";  
 RL J. Exp. Med. 187:237-244(1998).  
 RN [10]  
 RP 3D-STRUCTURE MODELING OF 24-144.  
 RX MEDLINE=97189482; PubMed=9037712;  
 RA Bajorath J., Aruffo A.;  
 RT "Construction and analysis of a detailed three-dimensional model of  
 RT the ligand binding domain of the human B cell receptor CD40.";  
 RL Proteins 27:59-70(1997).  
 RN [11]

RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber B., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 RT with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH  
 RP TRAF3.  
 RX MEDLINE=20442386; PubMed=10984535;  
 RA Ni C.Z., Welsh K., Leo E., Chlou C.K., Wu H., Reed J.C., Ely K.R.;  
 RT "Molecular basis for CD40 signaling mediated by TRAF3.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH  
 RP TRAF3.  
 RX MEDLINE=22000222; PubMed=12005438;  
 RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,  
 RA Satterthwait A.C., Cheng G., Ely K.R.;  
 RT "Downstream regulator TRAF3 binds to the CD40 recognition site on  
 RT TRAF3.";  
 RL Structure 10:403-411(2002).  
 RN [14]  
 RP VARIANT HIGM3 ARG-83.  
 RX MEDLINE=21532985; PubMed=11675497;  
 RA Ferrari S., Gilliani S., Insalaco A., Al-Chonaim A., Soresina A.R.,  
 RA Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,  
 RA Levy Y., Catalani N., Durandy A., Tbakhi A., Notarangelo L.D.,  
 RA Plebani A.;  
 RT "Mutations of CD40 gene cause an autosomal recessive form of  
 RT immunodeficiency with hyper IGM.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).  
 CC -!- FUNCTION: Receptor for TNFSF5/CD40L.  
 CC -!- SUSUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);  
 CC secreted (isoform II).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=I,  
 CC IsoId=P25942-1; Sequence=Displayed;  
 CC Name=II;  
 CC IsoId=P25942-2; Sequence=VSP\_006472, VSP\_006473;  
 CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.  
 CC -!- DISEASE: Defects in TNFRSF5 are the cause of hyper-IGM  
 CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an  
 CC autosomal recessive disorder which includes an inability of B  
 CC cells to undergo isotype switching, one of the final  
 CC differentiation steps in the humoral immune system, an inability  
 CC to mount an antibody-specific immune response, and a lack of  
 CC germinal center formation.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -!- DATABASE: NAME=PROT; NOTE=CD guide CD40 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".  
 CC -----  
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 CC -----  
 CC EMBL; X60592; CAA43045.1; --  
 CC EMBL; AL035662; CAC17670.1; --  
 CC EMBL; AJ300189; CAC29424.1; --  
 CC EMBL; BC012419; AAI12419.1; --  
 CC PIR; S04460; A60771.  
 CC PDB; 1CDF; 01-APR-97.  
 CC PDB; 1FLL; 18-OCT-00.  
 CC PDB; 1LOA; 08-FEB-00.  
 CC PDB; 1CZZ; 26-SEP-01.

FT	REPEAT	104	144	TNFR-CYS 3.
FT	REPEAT	145	187	TNFR-CYS 4.
FT	DISULFID	26	37	BY SIMILARITY.
FT	DISULFID	38	51	BY SIMILARITY.
FT	DISULFID	41	59	BY SIMILARITY.
FT	DISULFID	62	77	BY SIMILARITY.
FT	DISULFID	83	103	BY SIMILARITY.
FT	DISULFID	105	119	BY SIMILARITY.
FT	DISULFID	111	116	BY SIMILARITY.
FT	DISULFID	125	143	BY SIMILARITY.
FT	CARBOHYD	153	153	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	180	180	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	NON TER	269	269	
SEQ	SEQUENCE	269 AA;	746903F30F95F387	CRC64;

Query Match 61.1%; Score 558; DB 1; Length 269;  
Best Local Similarity 69.6%; Pred. No. 3,4e-44;  
Matches 94; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

QY	1	MVRPLQCLVWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTFTETEC	60
DB	1	MVRPLQCLFWGFLTAHSEPATACGEKQYPVNSLCDLCPFGQKLVNDCTEVSKTEC	60
QY	61	PCGSESEFLDTWNRETHCHQKQYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC	120
DB	61	SCGGEFLSTWNRKYCHEHRYCNPNLGLRIOSEGTINTDTTICVCEGQHTCSHTCES	120
QY	121	LHRSCSPGFGVKQIA	135
DB	121	PSLCLPFGFGVKQIA	135

RESULT 3  
TNR5 MOUSE STANDARD; PRT: 289 AA.  
ID TNR5 MOUSE STANDARD; PRT: 289 AA.  
AC P275I2; Q99NE0; Q99NE1; Q99NE2; Q99NE3;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 5 precursor  
GN (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDW40).  
DE TNR5F5 OR CD40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A. (ISOFORM I).  
RN MEDLINE=92105763; PubMed=1370315;  
RN Torres R.M., Clark E.A.;  
RN "Differential increase of an alternatively polyadenylated mRNA  
RN RT species of murine CD40 upon B lymphocyte activation.";  
RN J. Immunol. 148:620-626 (1992).  
RN [2]  
RN REVISIONS.  
RN STRAIN=BALB/c;  
RN Torres R.M.;  
RN Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A. (ISOFORM I).  
RN STRAIN=BALB/c; TISSUE=Liver;  
RN MEDLINE=93094586; PubMed=1281194;  
RN Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
RN Howard M., Cockayne D.A.;  
RN "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
RN J. Immunol. 149:3921-3926 (1992).  
RN [4]  
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND  
RN V).  
RN MEDLINE=21117110; PubMed=11172023;  
RN Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;  
RN "Regulation of CD40 function by its isoforms generated through  
RN alternative splicing.";

Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

[5] INTERACTION WITH TRAF3.

Medline=95184010; PubMed=7533327;

Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;

"Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";

Science 267:1494-1498(1995).

[6] INTERACTION WITH TRAF5.

Medline=96382484; PubMed=8790348;

Ischida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T., Yamamoto T., Inoue J.-I.;

TRAF5, a novel tumor necrosis factor receptor-associated factor family protein, mediates CD40 signaling.";

Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).

CC -!- FUNCTION: Receptor for TNFSP5/CD40L.

CC -!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1, TRAF2 and TRAF6 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV and V); secreted (isoform II).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=5;

CC Name=I;

CC IsoId=p27512-1; Sequence=Displayed;

CC Name=II;

CC IsoId=p27512-2; Sequence=VSP\_006474, VSP\_006475;

CC Name=III;

CC IsoId=p27512-3; Sequence=VSP\_006477, VSP\_006478;

CC Name=IV;

CC IsoId=p27512-4; Sequence=VSP\_006479, VSP\_006480;

CC Name=V;

CC IsoId=p27512-5; Sequence=VSP\_006476;

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL; M83312; AAB08705.1; .

EMBL; M94126; AAA37404.1; .

EMBL; M94129; AAA37404.1; JOINED.

EMBL; M94128; AAA37404.1; JOINED.

EMBL; M94127; AAA37404.1; JOINED.

EMBL; AJ401387; CAC29427.1; .

EMBL; AJ401388; CAC29428.1; .

EMBL; AJ401389; CAC29429.1; .

EMBL; AJ401390; CAC29430.1; .

PIR; A46476; A46476.

HSP; P25942; 1CDF.

MGD; MGI188336; TNfrsf5.

InterPro; IPR008063; Fas\_receptor.

InterPro; IPR001368; TNFR\_c6.

Pfam; PF00020; TNFR\_C6; 4.

PRINTS; PR01680; FASRECEPTOR.

SMART; SM00208; TNFR; 4.

PROSITE; PS00652; TNFR\_NGFR\_1; 1.

PROSITE; PS50050; TNFR\_NGFR\_2; 4.

Receptor; Transmembrane; Glycoprotein; Repeat; Signal;

Alternative splicing.

SIGNAL 1 19

CHAIN 20 289

POTENTIAL.

TUMOR NECROSIS FACTOR RECEPTOR

SUPERFAMILY MEMBER 5.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.

TNFR-CYS 5.

FT DISULFID 26 37 BY SIMILARITY.

FT DISULFID 38 51 BY SIMILARITY.

FT DISULFID 41 59 BY SIMILARITY.

FT DISULFID 62 77 BY SIMILARITY.

FT DISULFID 83 103 BY SIMILARITY.

FT DISULFID 105 119 BY SIMILARITY.

FT DISULFID 111 116 BY SIMILARITY.

FT DISULFID 125 143 BY SIMILARITY.

FT CARBOHYD 153 153 N-LINKED (GLCNAC... ) (POTENTIAL).

FT VARSPLIC 166 203 SCEDKLEVLQKQTSQTVICGLKSRMALIVPWVG -> RFPVDPASPGHSCRDGPHHHFRGVSLSYQGGQETKG (in isoform II).

FT /FTid=VSP\_006474.

FT Missing (in isoform II).

FT /FTid=VSP\_006475.

FT GLKSRMALIVPVVMGILITIFGVFLYIK -> E (in isoform V).

FT /FTid=VSP\_006476.

FT VARSPLIC 216 234 KKVVKPKDNEMLPFAARR -> SECSEEREFGFSPVEPA S (in isoform III).

FT /FTid=VSP\_006477.

FT Missing (in isoform III).

FT VARSPLIC 235 289 /FTid=VSP\_006478.

FT KKVVKKP -> SGOETKG (in isoform IV).

FT /FTid=VSP\_006479.

FT Missing (in isoform IV).

FT VARSPLIC 223 289 /FTid=VSP\_006480.

FT /FTid=VSP\_006480.

SQ SEQUENCE 289 AA; 32111 NW; C791CB6D2FEA574E CRC64;

Query Match 52.9%; Score 483; DB 1; Length 289;

Best Local Similarity 54.9%; Pred No. 2.6e-37;

Matches 79; Conservative 21; Mismatches 44; Indels 0; Gaps 0;

QY 1 MYRLPQLQVGLGCLLTAVHPPEPTACREKQYLINSQCSCLOPQKLVSDCTETETECL 60

Db 1 MVSFLCALMGCLLTAVHLGQVCTCSKQYLHDGQCDLQCGSRLTSHCTALEKTQCH 60

QY 61 PCGESEFLDTWNRETHCHQKXCDPNLGRVQOQGTSETDTICTCEGHWHTSACRSCV 120

Db 61 PCDSGEFSAQWNRREIRCHQHCEPNQGLRVKSGTASDTVCTCKGQHCTSKDCEACA 120

QY 121 LHRSCSPGFGVKQIAVRPKTWLCN 144

Db 121 QHTPCIPGFGVWENATETDTIVCH 144

RESULT 4

TR11 MOUSE

ID TR11 MOUSE STANDARD; PRT; 625 AA.

AC O35305; Q8VCT7;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-kB) (Osteoclast differentiation factor receptor) (ODFR).

DE TNFRSF11A OR RANK.

GN TNFRSF11A OR RANK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Petal liver;

RX MEDLINE=98032977; PubMed=9367155;

RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.;

RT "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";

RL Nature 390:175-179(1997).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodargren B.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smal  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=99097247; PubMed=9878548;  
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,  
RA Morinaga T., Higashio K.;  
RT "RANK is the essential signaling receptor for osteoclast  
RT differentiation factor in osteoclastogenesis";  
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).  
CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for  
CC RANKL-mediated osteoclastogenesis. Involved in the regulation of  
CC interactions between T-cells and dendritic cells.  
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: Ubiquitous EXPRESSION WITH HIGH LEVELS IN  
CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.  
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR ENBL; AF019046; AAB86810.1; -;  
DR ENBL; BC019185; AAB19185.1; -;  
DR HSSP; P25942; 1CDF.  
DR MGD; MG1:1314891; Tnfrsf11a.  
DR GO; GO:0007275; P:development; IMP.  
DR GO; GO:0007515; P:lymph gland development; IMP.  
DR GO; GO:0001503; P:ossification; IMP.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 625 TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 11A.  
FT DOMAIN 31 214 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 215 234 POTENTIAL.  
FT DOMAIN 235 625 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 35 69 TNFR-CYS 1.  
FT REPEAT 72 113 TNFR-CYS 2.  
FT REPEAT 115 152 TNFR-CYS 3.  
FT REPEAT 155 195 TNFR-CYS 4.  
FT DISULFID 35 47 BY SIMILARITY.

FT DISULFID 48 61 BY SIMILARITY.  
FT DISULFID 51 69 BY SIMILARITY.  
FT DISULFID 72 87 BY SIMILARITY.  
FT DISULFID 93 113 BY SIMILARITY.  
FT DISULFID 115 128 BY SIMILARITY.  
FT DISULFID 134 152 BY SIMILARITY.  
FT CARBOHYD 106 106 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 175 175 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CONFLICT 494 494 R -> K (IN REF. 2).  
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;  
Query Match 28.7%; Score 262; DB 1; Length 625;  
Best Local Similarity 38.2%; Pred. No. 9.6e-17;  
Matches 52; Conservative 16; Mismatches 66; Indels 2; Gaps 2;  
QY 8 CVLVGCLLTAVHPPTACREKQVLYNSQCSCSLCOPQKLVSDCTETETELCPGSEF 67  
Db 19 CVLVLPVQVTLQVTPP-CTQERHYEHLGRCCSRCEPKYLSKCTPTSDSVCLPCCGDEY 77  
QY 68 LDTWNRETHCHQHKYCDPNTGLRVQOQKGTSETDTCTCEEGWCHTSPACSSVLHRCSP 127  
Db 78 LDTWNEEDKCLLHKVCDAGKALVAVDPGNHTAPPRCACTAGYHWNSD-CCECRRTTECAP 136  
QY 128 GFGYKQIAVRPKTWLC 143  
Db 137 GFGAQLPLQLNKOTVC 152  
RESULT 5  
TR111 HUMAN STANDARD; PRT; 616 AA.  
AC Q976Q6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 11A precursor  
DE (Receptor activator of NF-kB) (Osteoclast differentiation factor  
DE receptor) (CDPR).  
GN TNFRSF11A OR RANK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Dendritic cell;  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
RT and dendritic-cell function";  
RL Nature 390:175-179(1997).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=99097247; PubMed=9878548;  
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,  
RA Morinaga T., Higashio K.;  
RT "RANK is the essential signaling receptor for osteoclast  
RT differentiation factor in osteoclastogenesis";  
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).  
RN [3]  
RP INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.  
RX MEDLINE=98447691; PubMed=9774460;  
RA Wong B.R., Josien R., Lee S.Y., Volgodskaya M., Steinman R.M.,  
RA Choi Y.;  
RT "The TRAF family of signal transducers mediates NF-kappaB activation  
RT by the TRANCE receptor";  
RN J. Biol. Chem. 273:28355-28359(1998).  
RN [4]  
RP VARIANT FEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2  
RP ALA-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.  
RX MEDLINE=20082806; PubMed=10615125;

RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,  
 RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,  
 RA Anderson D.M.;  
 RT "Mutations in TNFRSF11A affecting the signal peptide of RANK, cause  
 RT familial expansile osteolysis.";  
 RL Nat. Genet. 24:45-48(2000).  
 CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANSC/OPGL; essential for  
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of  
 CC interactions between T-cells and dendritic cells.  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in  
 CC skeletal muscle, thymus, liver, colon, small intestine and adrenal  
 CC gland.  
 CC -!- DISEASE: Defects in TNFRSF11A are the cause of familial expansile  
 CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant  
 CC bone disorder characterized by focal areas of increased bone  
 CC remodelling. The osteolytic lesions develop usually in the long  
 CC bones during early adulthood. FEO is often associated with early  
 CC onset deafness and loss of dentition.  
 CC -!- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone  
 CC 2 (PDB2) [MIM:602080]; also known as familial Paget disease of  
 CC bone. PDB2 is a bone remodelling disorder with clinical  
 CC similarities to FEO. Unlike FEO, however, affected individuals  
 CC have involvement of the axial skeleton with lesions in the spine,  
 CC pelvis and skull.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; AF018253; AAB86809.1; -.  
 DR HSSP; P25942; 1CDF.  
 DR Genew; HGNC:11908; TNFRSF11A.  
 DR MIM; 603499; -.  
 DR MIM; 174810; -.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS0050; TNFR\_NGFR\_2; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;  
 KW Disease mutation; Deafness.  
 FT SIGNAL 1 29 POTENTIAL  
 FT CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR  
 FT SUPERFAMILY MEMBER 11A.  
 FT DOMAIN 30 212 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 213 233 POTENTIAL.  
 FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 34 68 TNFR-CYS 1.  
 FT REPEAT 71 112 TNFR-CYS 2.  
 FT REPEAT 114 151 TNFR-CYS 3.  
 FT REPEAT 154 194 TNFR-CYS 4.  
 FT REPEAT 34 46 BY SIMILARITY.  
 FT DISULFID 47 60 BY SIMILARITY.  
 FT DISULFID 50 68 BY SIMILARITY.  
 FT DISULFID 71 86 BY SIMILARITY.  
 FT DISULFID 92 112 BY SIMILARITY.  
 FT DISULFID 114 127 BY SIMILARITY.  
 FT DISULFID 133 151 BY SIMILARITY.  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT VARIANT 21 21 L -> LALLLCALL (in PDB2).

FT VARIANT 21 21 /FTID=VAR\_011516.  
 FT L -> LLLCALL (in FEO).  
 FT /FTID=VAR\_011517.  
 FT A -> V.  
 FT /FTID=VAR\_011518.  
 SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;  
 Query Match 28.4%; Score 259; DB 1; Length 616;  
 Best Local Similarity 37.9%; Pred. No. 1.8e-16;  
 Matches 53; Conservative 17; Mismatches 68; Indels 2; Gaps 2;  
 QY 4 LPLOCVLWCLLTAVHPPTACREKQYLINSQCCLSQPGKLVSDCTETETECPLCG 63  
 Db 14 LLLLCALLARLQVALQIAPP-CTSEKHYEHLGRNCNCKECPGKYMSKCTTTSDSVCLPCG 72  
 QY 64 ESEFDTWNRETHCHQHKYCDPNLGRVQQKGTSETDITCTCEGWHCTSEACSCVLHR 123  
 Db 73 PDEYLDWNNEEDKLLHKVCDTGKALVAVAGNSTTPRCAC TAGYH-WSQDCCCRNT 131  
 QY 124 SCSPGFGVKQIAVRPKTWLC 143  
 Db 132 ECAPGLGAQHPLQLNKDTVC 151  
 RESULT 6  
 TRIB\_HUMAN STANDARD; PRT; 461 AA.  
 ID TRIB\_HUMAN STANDARD; PRT; 461 AA.  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor  
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Stanercept)  
 DE [Contains: Tumor necrosis factor binding protein 2 (TNFII)].  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT ARG-196.  
 RX MEDLINE=91045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; PubMed=8661109;  
 RA Beltlinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:94-100(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND  
 RP ARG-301.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PNS;

RA MEDLINE=22388257; PubMed=12477932;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Altshuler S.F., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
RA Hopkins R.F., Jordan H., Moore J., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RL human and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [6]  
RP SEQUENCE OF 37-461 FROM N.A.  
RX MEDLINE=91370690; PubMed=1966549;  
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,  
RT "Two human TNF receptors have similar extracellular, but distinct  
RT intracellular, domain sequences."  
RL Cytokine 2:231-237 (1990).  
RN [7]  
RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.  
RX MEDLINE=90349572; PubMed=2166946;  
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
RA Ringold G.M.;  
RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
RT and demonstration of a shed form of the receptor."  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155 (1990).  
RN [8]  
RP SEQUENCE OF 154-193 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21069356; PubMed=1197692;  
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;  
RT "New single nucleotide polymorphisms in the coding region of human  
RT TNFR2: association with systemic lupus erythematosus."  
RL Genes Immun. 1:501-503 (2000).  
RN [9]  
RP SEQUENCE OF 27-31.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors."  
RL J. Biol. Chem. 265:1531-1536 (1990).  
RN [10]  
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
RX MEDLINE=91056048; PubMed=2173696;  
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
RA Brockhaus M.;  
RT "Purification and partial amino acid sequence analysis of two  
RT distinct tumor necrosis factor receptors from HL60 cells."  
RL J. Biol. Chem. 265:20131-20138 (1990).  
RN [11]  
RP CHARACTERIZATION.  
RX MEDLINE=93016040; PubMed=1328224;  
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
RA Lipari M.T., Goeddel D.V.;  
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
RT Characterization of ligand binding, internalization, and receptor  
RT phosphorylation."  
RL J. Biol. Chem. 267:21172-21178 (1992).  
RN [12]  
RP INTERACTION WITH TRAF2.  
RX MEDLINE=94349371; PubMed=8069916;  
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;  
RT "A novel family of putative signal transducers associated with the  
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor."  
RL Cell 78:681-692 (1994).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
RX TRAF2.  
RX MEDLINE=99221490; PubMed=10206649;  
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
RT "Structural basis for self-association and receptor recognition of  
RT human TRAF2."  
RL Nature 398:533-538 (1999).  
RN [14]  
RP VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21603989; PubMed=11762942;  
RA Morita C., Horiuchi T., Tsukamoto H., Hatta N., Kikuchi Y.,  
RA Arinobu Y., Otsuka T., Sawabe T., Harashina S., Nagasawa K., Niho Y.;  
RT "Association of tumor necrosis factor receptor type II polymorphism  
RT 196R with systemic lupus erythematosus in the Japanese: molecular and  
RT functional analysis."  
RL Arthritis Rheum. 44:2819-2827 (2001).  
RN [15]  
RP VARIANT ARG-196.  
RX MEDLINE=22151311; PubMed=12161545;  
RA Peral B., San Millan J.L., Castello R., Moghetti P.,  
RA Escobar-Morreale H.F.;  
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the  
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic  
RT ovary syndrome and hyperandrogenism."  
RL J. Clin. Endocrinol. Metab. 87:3977-3983 (2002).  
CC -!- FUNCTION: Receptor with high affinity for homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the  
CC apoptotic suppressors BIRC2 and BIRC3 to TNFSF1B/TNFR2. The TNF  
CC receptor 2 mediates most of the metabolic effects of TNF-alpha.  
CC -!- SUBUNIT: Binds to TRAF2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- PTM: Phosphorylated; mainly on serine residues and with a very low  
CC level on threonine residues.  
CC -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is  
CC produced from the membrane form by proteolytic processing.  
CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and  
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid  
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding  
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to  
CC TNF-alpha and blocks its interactions with receptors.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- DATABASE: NAME=PROX; NOTE=CD guide CD120b entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"  
CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
CC WWW="http://www.enbrel.com/"

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; M32315; AAC59929.1; -  
DR EMBL; U52165; AAC50622.1; -  
DR EMBL; U52156; AAC50622.1; JOINED.  
DR EMBL; U52157; AAC50622.1; JOINED.  
DR EMBL; U52158; AAC50622.1; JOINED.  
DR EMBL; U52159; AAC50622.1; JOINED.  
DR EMBL; U52160; AAC50622.1; JOINED.  
DR EMBL; U52161; AAC50622.1; JOINED.  
DR EMBL; U52162; AAC50622.1; JOINED.  
DR EMBL; U52163; AAC50622.1; JOINED.  
DR EMBL; U52164; AAC50622.1; JOINED.  
DR EMBL; M55994; AAA36755.1; -  
DR EMBL; AY264804; AAO89076.1; -  
DR EMBL; AY342040; AAP89939.1; -

DR EMBL; BC052977; AAH52977.1; --  
DR EMBL; S63368; AAL19824.2; --  
DR EMBL; M35857; AAA63262.1; --  
DR EMBL; AB030950; BAA89053.1; --  
DR PIR; A33356; A33356.  
DR PDB; 1CA9; 12-APR-99.  
DR Genew; HGNC:11917; TNFRSF1B.

Query Match 23.3%; Score 212.5; DB 1; Length 461;  
Best Local Similarity 34.5%; Pred. No. 2.4e-12;  
Matches 51; Conservative 12; Mismatches 58; Indels 27; Gaps 6;  
QY 4 LPQCVMGCLLTAVHPPTACREKQVLYNS--CCSLCQPGQKLVSDCTETETECPLP 61  
DB 23 LPAQVA-----FTYAPPGSTCLREYDQTAQCCSKSPGQAKVFTKTSIDVDCDS 77  
QY 62 CGSEBELDTWRETHCHQHKYCDNLGLRVQ-----QKGTSETDTTCTCEGWHCT--- 112  
DB 78 CEDSTYTLQNMWVPEC-----LSCSRCSSDQVETQACTREONRICTCRPGWYCALSK 130  
QY 113 SEACESCVLHRCSPGFGVKQIAVRPKT 140  
DB 131 QEGCLCAPLKCPRGFGV-----ARPGT 154

RESULT 7  
TR14 HUMAN  
ID TR14 HUMAN STANDARD; PRT; 283 AA.  
AC Q92956; OSWXR1; Q96J31; Q9UM65;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 14 precursor  
DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)  
DE (TR2).  
GN TNFRSF14 OR HVEM OR HVEM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cervical adenocarcinoma;  
RX MEDLINE=97053782; PubMed=8898196;  
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;  
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of  
RL the TNF/NGF receptor family.";  
RN Cell 87:427-436(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97306336; PubMed=9162061;  
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,  
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,  
RA Porter T.G., Truneh A., Young P.R.;  
RT "A newly identified member of the tumor necrosis factor receptor  
superfamily with a wide tissue distribution and involvement in  
RT lymphocyte activation";  
RL J. Biol. Chem. 272:14272-14276(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Zhang W., Wan T., Cao X.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. AND VARIANTS ARG-17 AND ILE-241.  
RX MEDLINE=21629477; PubMed=11756979;  
RA Struyf F., Posavard C.M., Keyaerts E., Van Ranst M., Corey L.,  
RA Spear P.G.;  
RT "Search for polymorphisms in the genes for herpesvirus entry mediator,  
Nectin-1, and Nectin-2 in immune seronegative individuals.";  
RL J. Infect. Dis. 185:36-44(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;

RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Botterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RX INTERACTION WITH TRAF2 AND TRAF5.  
RX MEDLINE=97298041; PubMed=9153189;  
RA Hsu H., Solovvey I., Colombero A., Elliott R., Kelley M., Boyle W.J.;  
RT "ATAR, a novel tumor necrosis factor receptor family member, signals  
through TRAF2 and TRAF5.";  
RL J. Biol. Chem. 272:13471-13474(1997).  
RN [7]  
RX INTERACTION WITH TRAF3 AND TRAF5.  
RX MEDLINE=97306297; PubMed=9162022;  
RA Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,  
RA Ashkenazi A.;  
RT "Herpesvirus entry mediator, a member of the tumor necrosis factor  
receptor (TNFR) family, interacts with members of the TNFR-associated  
factor family and activates the transcription factors NF-kappaB and  
AP-1.";  
RL J. Biol. Chem. 272:14029-14032(1997).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.  
RX MEDLINE=21403268; PubMed=11511370;  
RA Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,  
RA Eisenberg R.J., Wiley D.C.;  
RT "Herpes simplex virus glycoprotein D bound to the human receptor  
HveA.";  
RL Mol. Cell 8:169-179(2001).  
CC -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric  
TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays  
an important role in HSV pathogenesis because it enhanced the  
entry of several wildtype HSV strains of both serotypes into CHO  
cells, and mediated HSV entry into activated human T cells.  
CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION  
IN LUNG, SPLEEN, AND THYMUS.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC  
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CC  
CC EMBL; U70321; AAB58354.1; --  
CC EMBL; U81232; AAD00505.1; --  
CC EMBL; AF153978; AAF75588.1; --  
CC EMBL; AF373877; AAL47717.1; --  
CC EMBL; AF373878; AAL47718.1; --  
CC EMBL; BC002794; AAH02794.1; --  
CC PDB; 1JXA; 26-SEP-01.  
CC Genew; HGNC:11912; TNFRSF14.

DR MIM; 602746; .  
DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.  
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
DR GO; GO:0006955; P:immune response; TAS.  
DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR PRINTS; PRO1680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 2.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;  
KW 3D-structure.  
FT SIGNAL 1 38  
FT CHAIN 39 283  
FT DOMAIN 39 202  
FT TRANSMEM 203 223  
FT DOMAIN 224 283  
FT REPEAT 42 75  
FT REPEAT 78 119  
FT REPEAT 121 162  
FT DISULFID 42 53  
FT DISULFID 54 67  
FT DISULFID 57 75  
FT DISULFID 78 93  
FT DISULFID 96 111  
FT DISULFID 99 119  
FT DISULFID 121 138  
FT DISULFID 127 135  
FT CARBOHYD 110 110  
FT CARBOHYD 173 173  
FT VARIANT 17 17  
FT VARIANT 241 241  
FT TURN 44 45  
FT STRAND 46 46  
FT STRAND 49 49  
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FT STRAND 55 55  
FT STRAND 57 57  
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FT STRAND 61 65  
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FT TURN 80 81  
FT STRAND 82 83  
FT STRAND 86 88  
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FT STRAND 105 109  
FT STRAND 118 121  
FT TURN 123 124  
FT STRAND 125 129  
FT STRAND 137 140  
SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;  
  
Query Match 22.1%; Score 202; DB 1; Length 283;  
Best Local Similarity 29.1%; Pred. No. 1.4e-11;  
Matches 43; Conservative 26; Mismatches 69; Indels 10; Gaps 3;  
  
QY 1 MVLPLQCVLWG--CLLTAVHPFPACREKQYLINSQCCLSQCGQKLVSDCTFTTTE 58  
Db 20 VLRLVLYLFTLGPAPCAPAL-----PSCKEDBYPVGVSECCPKCSFGYRVEACGELTGV 74  
QY 59 CLPCGSESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWEC---TSEA 115  
Db 75 CBPCPPTTIAHLNGLSKLCLQCMQCDPAMGLRARNCSRTENAVCCSPGHCFTIVQDGH 134  
QY 116 CRSCVLHRSRCSFGYKQIAVRPKTWLC 143  
Db 135 CAACRAYATSSPGQRVOKGKGTSDTLG 162

RESULT 8  
TNR3\_HUMAN STANDARD; PRT; 435 AA.  
ID TNR3\_HUMAN P36941;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
DE (lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related  
DE protein) (Tumor necrosis factor C receptor).  
GN LTR OR TNFSF3 OR TNFR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93252381; PubMed=8486360;  
RA Baens W., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
RA "Construction and evaluation of a hncDNA library of human l2p  
RA transcribed sequences derived from a somatic cell hybrid.";  
RA Genomics 16:214-218(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22386257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshnyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length  
RA human and mouse cDNA sequences";  
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=94225209; PubMed=8171323;  
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,  
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
RA "A lymphotoxin-beta-specific receptor.";  
RA Science 264:707-710(1994).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=99223511; PubMed=10207006;  
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;  
RA "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell  
RA death in HeLa cells.";  
RA J. Biol. Chem. 274:11868-11873(1999).  
RN [5]  
RP FUNCTION.  
RX MEDLINE=20261554; PubMed=10799510;  
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,  
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;  
RA "The lymphotoxin-beta receptor is necessary and sufficient for  
RA LIGHT-mediated apoptosis of tumor cells.";  
RA J. Biol. Chem. 275:14307-14315(2000).  
RN [6]  
RP INTERACTION WITH TRAF3.

RX MEDLINE=96278943; PubMed=8663299;  
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
 RA Yagita H., Okumura K.;  
 RT "TRAFs, an activator of NF-kappaB and putative signal transducer for  
 RT the lymphotoxin-beta receptor.";  
 RL J. Biol. Chem. 271:14661-14664(1996).  
 RN [7]  
 RP INTERACTION WITH TRAF4.  
 RX MEDLINE=96289299; PubMed=9626059;  
 RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,  
 RA Gascayne R.D., Beren K., McFadden D., Shabal A., Hugh J.,  
 RA Reynolds A., Clevenger C.V., Reed J.C.;  
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal  
 RT adult, fetal, and tumor tissues";  
 RL Am. J. Pathol. 152:1549-1561(1998).  
 RN [8]  
 RP INTERACTION WITH TRAF5.  
 RX MEDLINE=98172745; PubMed=9511754;  
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,  
 RA Otsuka M., Yamamoto T., Inoue J.-I.;  
 RT "Cloning and characterization of a cDNA encoding the human homolog of  
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
 RL Gene 207:135-140(1998).  
 CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
 CC LTA and LTb, and for TNFalpha/LIGHT. Promotes apoptosis via TRAF3  
 CC and TRAF5. May play a role in the development of lymphoid organs.  
 CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -----  
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 CC -----  
 CC ENBL; L04270; AAA36757.1; -.  
 DR EMBL; BC026262; AAH26262.1; -.  
 DR PIR; I54182; I54182.  
 DR HSP; P25942; LCDF.  
 DR Genew; HGNC:6718; LTBR.  
 DR MIN; 600979; -.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR008063; Fas receptor.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR NGFR\_1; 2.  
 DR PROSITE; PS00650; TNFR NGFR\_2; 3.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 435  
 FT DOMAIN 31 227  
 FT TRANSMEM 228 248  
 FT DOMAIN 249 435  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 168  
 FT REPEAT 169 211  
 FT DISULFID 43 58  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 148  
 FT DISULFID 142 167  
 FT DISULFID 170 185

FT CARBOHYD 40 40 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 177 177 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;  
 Query Match 21.9%; Score 200; DB 1; Length 435;  
 Best Local Similarity 36.5%; Pred. No. 3.2e-11;  
 Matches 50; Conservative 15; Mismatches 58; Indels 14; Gaps 6;  
 QY 5 PLQCVLWGCILTAHVPE--PTTA-----CR--EKQYLINSQ--CCSLCQPCQKLVSCDTE 53  
 DB 16 PLVLGLFG-LLAASQPAVPPYASENQTCDQEKYEYEPQHRICCSRCPPTGYVSAKCSR 74  
 QY 54 FTEETCLPGSGSEFLDTWRNETHQHVKYCDPNLGLRVQOKGTSETTICTCEEGMHTCS 113  
 DB 75 IRDIVCATCAENSYNENHWNVLTICQLGCPDPVWGLBEIAPCTSKRKTQCCQFQGMCAA 134  
 QY 114 EA--CESCVLHRSCLSPG 128  
 DB 135 WALECTHCELLSDCPG 151  
 RESULT 9  
 TNR6 RAT  
 ID TNR6 RAT STANDARD; PRT; 324 AA.  
 AC Q63199;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL  
 DE receptor) (Apoptosis-mediating surface antigen Fas) (Apo-1 antigen;  
 DE (CD95)).  
 GN TNFRSF6 OR P11 OR FAS.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RC MEDLINE=94128114; PubMed=7507668;  
 RA Kimura K., Yamamoto M., Wakatsuki T.;  
 RT "A variant mRNA species encoding a truncated form of Fas antigen in  
 RL the rat liver.";  
 RL Biochem. Biophys. Res. Commun. 198:666-674(1994).  
 CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD  
 CC recruits caspase-8 to the activated receptor. The resulting death-  
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
 CC activation which initiates the subsequent cascade of caspases  
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
 CC mediated apoptosis may have a role in the induction of peripheral  
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or  
 CC both (By similarity).  
 CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 CC -----  
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 CC -----  
 CC EMBL; D26112; BAA05108.1; -.  
 DR PIR; JC2395; JC2395.  
 DR HSP; P25445; 1DDF.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR008063; Fas\_receptor.  
 DR InterPro; IPR001368; TNFR\_c6.

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DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 324
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 6.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 172 188
FT DOMAIN 172 188
FT DOMAIN 189 324
FT REPEAT 43 79
FT REPEAT 80 123
FT REPEAT 124 163
FT DOMAIN 219 303
FT DISULFID 44 55
FT DISULFID 56 69
FT DISULFID 59 78
FT DISULFID 81 97
FT DISULFID 100 115
FT DISULFID 103 123
FT DISULFID 125 139
FT DISULFID 142 154
FT CARBOHYD 43 43
FT CARBOHYD 114 114
FT CARBOHYD 132 132
FT SEQUENCE 324 AA; 36835 MW; D2SD583C909D9D09 CRC64;
Query Match 20.6%; Score 188.5; DB 1; Length 324;
Best Local Similarity 30.6%; Pred. No. 2.7e-10;
Matches 44; Conservative 20; Mismatches 69; Indels 11; Gaps 5;
QY 21 EPTACREKQYLINQCCSLCOPGOKLYSDC-TEETETECPCGE-SFELDTWNRETHCH 78
DB 39 ETDNNCSGLYGVGFQPCQPGGRKVKDCTSGGAPCTGEGBYDRKHVYDKCR 98
QY 79 QHKYCDPNLGLRVQOKGSETDTITCTCEGWHCTSEACESCVLHRSCTSPGFGVKQI---A 135
DB 99 RCAFCDEGHGLEVEINRTQNTKCKENFYCNASLDCDHCYHCTSC---GLEDLLEPC 154
QY 136 VPKTWLCNRQAT--RLMLSVVP 157
DB 155 TETSTKCKKQSSNYKLLWLLLP 178
RESULT 10
ID T11B_RAT STANDARD; PRT; 401 AA.
AC 008727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luehth R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Clegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
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RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RL Cell 89:309-319(1997).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Upregulated by osteopontin.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 2 death domains.
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CC or send an email to license@isb-sib.ch).
DR EMBL; U94330; AAB53707.1; -.
DR HSSP; P25942; 1CDF.
DR InterPro; IPR000486; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 11B.
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT SEQUENCE 401 AA; 46192 MW; FEC6A31F1DAE573A CRC64;
Query Match 19.8%; Score 181; DB 1; Length 401;
Best Local Similarity 32.3%; Pred. No. 1.6e-09;
Matches 42; Conservative 17; Mismatches 55; Indels 16; Gaps 5;
QY 18 VHPPTACREKQYLINQCCSLCOPGOKLYSDC-TEETETECPCGESEFLDTWNRETHC 77
DB 29 LHYDPTG---RQLL-----CDKCAPGTLYKQCTVRRKTLVCPGPDYSYDTSWHTSDEC 80
QY 78 HQHKYCDPNLGL--LRVQOKGTSSTDTICTCEGWHCTSEACESCVLHRSCTSPGFGVKQIA 135
DB 81 ---VYCSFVKELQTVKQECNRTNVRVCECEGRYL---ELEFLKHSRSCFPGVLQAG 134
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QY 136 VRPKWLCNR 145  
DB 135 TPERNVCKR 144

RESULT 11  
TNR6 MOUSE STANDARD; PRT; 327 AA.  
AC P25436; Q9DCQ1;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL)  
DE Receptor (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)  
DE (CD95).  
GN TNFRSF6 OR APT1 OR FAS.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[3]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=92148151; PubMed=1371136;  
RX Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,  
RA Copeland N.G., Jenkins N.A., Nagata S.;  
RA "The cDNA structure, expression, and chromosomal assignment of the  
RT mouse Fas antigen.";  
RL J. Immunol. 148:1274-1279 (1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/Sv;  
RA Koczan D., Ibrahim S.M., Thiesen H.J.;  
RT "Role of a mutant fas receptor in a transgenic mouse.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; Tissue=Kidney;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Giasi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
RN [4]  
RP SEQUENCE OF 1-96 FROM N.A.  
RX MEDLINE=93189576; PubMed=7680478;  
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;  
RT "Aberrant transcription caused by the insertion of an early  
RT transposable element in an intron of the Fas antigen gene of lpr  
RT mice.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760 (1993).  
RN [5]  
RP INTERACTION WITH DAXX.  
RX MEDLINE=97358533; PubMed=9215629;  
RX Yang X., Khosravi-Far R., Chang H.Y., Baltimore D.;  
RT "Daxx, a novel Fas-binding protein that activates JNK and apoptosis.";  
RL Cell 89:1067-1076 (1997).  
RN [6]

VARIANT LPR.  
RX MEDLINE=92195401; PubMed=1372394;  
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,  
RA Nagata S.;  
RT "Lymphoproliferation disorder in mice explained by defects in Fas  
RT antigen that mediates apoptosis.";  
RL Nature 356:314-317 (1992).  
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD  
CC recruits caspase-8 to the activated receptor. The resulting death-  
CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
CC activation which initiates the subsequent cascade of caspases  
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
CC mediated apoptosis may have a role in the induction of peripheral  
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or  
CC both (By similarity).  
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,  
CC LIVER, LUNG, HEART, AND ADULT OVARY.  
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -!- DISEASE: Defects in TNFRSF6 are the cause of the  
CC lymphoproliferation phenotype (lpr). Lpr mice show lymphadenopathy  
CC and autoantibody production.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -----  
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CC -----  
CC EMBL; M83649; AAA37593.1; -;  
CC EMBL; AK002590; BAB2211.1; -;  
CC EMBL; AJ295702; CAC00638.1; -;  
CC EMBL; AJ295703; CAC00638.1; JOINED.  
CC EMBL; AJ295704; CAC00638.1; JOINED.  
CC EMBL; S56490; AAB25700.1; -;  
CC EMBL; S56485; AAB25700.1; JOINED.  
CC EMBL; S56486; AAB25700.1; JOINED.  
CC PIR; A46484; A46484.  
CC HSSP; P25445; 1DDF.  
CC MGD; MGI:95484; Tnfrsf6.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR008063; Fas\_receptor.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00020; TNFR\_c6; 3.  
CC PRINTS; PR01580; FASRECEPTOR.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00208; TNFR; 3.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
CC PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
CC PROSITE; PS00017; DEATH\_DOMAIN; 1.  
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
CC Disease mutation.  
KW SIGNAL 1 21  
KW CHAIN 22 327  
FT FT  
FT DOMAIN 22 169 TUMOR NECROSIS FACTOR RECEPTOR  
FT TRANSMEM 170 186 SUPERFAMILY MEMBER 6.  
FT DOMAIN 187 327 EXTRACELLULAR (POTENTIAL).  
FT REPEAT 43 79 POTENTIAL.  
FT REPEAT 80 123 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 124 162 TNFR-CYS 1.  
FT REPEAT 162 306 TNFR-CYS 2.  
FT DOMAIN 222 306 TNFR-CYS 3.  
FT DISULFID 44 55 DEATH.  
FT DISULFID 56 69 BY SIMILARITY.  
FT DISULFID 59 78 BY SIMILARITY.  
FT DISULFID 81 97 BY SIMILARITY.

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FT DISULFID 100 115 BY SIMILARITY.
FT DISULFID 103 123 BY SIMILARITY.
FT DISULFID 125 139 BY SIMILARITY.
FT DISULFID 142 153 BY SIMILARITY.
FT DISULFID 145 161 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 I -> N (IN LPR). 3).
FT VARIANT 38 38 H -> R (IN REF. 3).
FT CONFLICT 38 38
SQ SEQUENCE 327 AA; 37418 MW; F6BFFC5ACE356EEE CRC64;

Query Match
Best Local Similarity 33.6%; Pred. No. 1.6e-09;
Matches 49; Conservative 15; Mismatches 68; Indels 14; Gaps 6;

QY 18 VPEPPTACREKQYLINQCCSLQCPGQKLVSDCTETET-BCLPCGB-SFELDTWNET 75
Db 37 VH-ETDKQKSEGLYGGPFCCQPCQFGKKKVEDCKWNGGTETCAPCTGKREYMDKNHYAD 95
QY 76 HCHOHKYCDPNGLRVOOKGTSETDTICTCEGHWCTSEACESCVLHRSQSPGFGVKQIA 135
Db 96 KCRRTLCDSEHGLEVETNCTITQNTKCKKDFCDSPGCEHCVRCSCEHG-----T 149
QY 136 VEPKWTWLV-----CNROA-QTRMLSLV 156
Db 150 LEPCTATNTNCRKQSPRNLWLTII 175

RESULT 12
TILB HUMAN
ID TILB HUMAN STANDARD; PRT; 401 AA.
AC O00300; C60236; 09UHP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11b precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPB OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wodden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RN Endocrinology 139:1329-1337(1998).
RN [3]
SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE=9688283; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RA "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";

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RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor.";
RN Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN [6]
RP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
RN Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN [7]
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis.";
RN Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN [8]
RP TRAIL BINDING.
RX MEDLINE=98263100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RN J. Biol. Chem. 273:14363-14367(1998).
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.;
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor.";
RN J. Biol. Chem. 273:5117-5123(1998).
RN [10]
RP REVIEW.
RX MEDLINE=21395914; PubMed=11505389;
RA Hofbauer L.C., Neuberger A., Heufelder A.E.;
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases.";
RL Cancer 92:460-470(2001).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of

```



its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta, and in embryo.

CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7, whereas expression decreases at day 11 and increases from day 15 to 17. On day 15 found in developing bone primordia, brachiocephalic artery and ductus arteriosus, left main bronchus, abdominal aorta and midgut.

CC -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by 1,25-dihydroxyvitamin D3 and parathyroid hormone.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 2 death domains.

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CC -----

DR EMBL; U94331; AAB53708.1; --

DR EMBL; AB013898; BAA28269.1; --

DR EMBL; AB013903; BAA33388.1; --

DR EMBL; AB013899; BAA33388.1; JOINED.

DR EMBL; AB013900; BAA33388.1; JOINED.

DR EMBL; AB013901; BAA33388.1; JOINED.

DR EMBL; AB013902; BAA33388.1; JOINED.

DR HSSP; P25942; 1CDF.

DR GGD; MG1:09587; Tnfrsf11b.

DR GO; GO:0005578; C:extracellular matrix; IDA.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR\_NGFR.2; 2.

DR Pfam; PF00020; TNFR\_c6; 3.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00017; DEATH\_DOMAIN; 1.

DR PROSITE; PS00652; TNFR\_NGFR.1; 1.

DR PROSITE; PS00050; TNFR\_NGFR.2; 2.

DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

KW SIGNAL 1 21 BY SIMILARITY.

FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR

FT SUPERFAMILY MEMBER 11B.

FT REPEAT 24 62 TNFR-CYS 1.

FT REPEAT 65 105 TNFR-CYS 2.

FT REPEAT 107 142 TNFR-CYS 3.

FT REPEAT 145 185 TNFR-CYS 4.

FT DOMAIN 198 269 DEATH 1.

FT DOMAIN 283 365 DEATH 2.

FT SITE 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).

FT DISULFID 41 54 BY SIMILARITY.

FT DISULFID 44 62 BY SIMILARITY.

FT DISULFID 65 80 BY SIMILARITY.

FT DISULFID 83 97 BY SIMILARITY.

FT DISULFID 87 105 BY SIMILARITY.

FT DISULFID 107 118 BY SIMILARITY.

FT DISULFID 124 142 BY SIMILARITY.

FT DISULFID 145 160 BY SIMILARITY.

FT DISULFID 166 185 BY SIMILARITY.

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 138 138 R->P (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).

FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 19.28; Score 175; DB 1; Length 401;

Best Local Similarity 30.08; Pred.No. 5.7e-09;

Matches 39; Conservative 18; Mismatches 57; Indels 16; Gaps 4;

QY 18 VHPPEPTACREKQYLINSQCCLCPGQKLVSDCTETETECPLCGESEFLDTWNRTHC 77

Db 29 LHYDPEFG-----HOLLCDKCAPGTLYKQHTVRRKTLCPGCPDHSYDTSWHTSDEC 80

QY 78 HQHYKCDPNLG--LRVQOKGTSETDICTCEGWHCTSEACECVLHRSCTPGGVKQIA 135

Db 81 ---VYCSFVCKELQSVKQECNTRNRYCECEGRYL---EIFCLKHRSCPPGSGVVQAG 134

QY 136 VRPKTWLCNR 145

Db 135 TPERNTVCKK 144

RESULT 14

TR1B MOUSE

ID TR1B MOUSE STANDARD; PRT; 474 AA.

AC P25119; P97893;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNF-R2) (p75).

GN TNFRSF1B OR TNFR2 OR TNFR-2.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9118785; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.;

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific."

RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91246168; PubMed=1645445;

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."

RL Mol. Cell. Biol. 11:3020-3026(1991).

RN [3]

RP SEQUENCE OF 1-26 FROM N.A.

RC STRAIN=NOJ;

RA Jacob C.O., Liu J.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 1-22 FROM N.A.

RC TISSUE=Liver;

RA Kissinger M., Fellows R., Feldmann M., Chernajovsky Y.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By similarity).



Search completed: July 21, 2004, 10:05:59  
Job time : 13 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2004, 10:03:04 ; Search time 39 Seconds  
(without alignments)  
1294.434 Million cell updates/sec

Title: US-10-031-607-7  
Perfect score: 913  
Sequence: 1 MVRFLQCVLWGLLTAVHP.....WLCNRQAQTRMLSVPRIG 160

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_archaea:\*  
2: SP\_bacteria:\*  
3: SP\_fungi:\*  
4: SP\_human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_organalle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP Vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_virus:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	785	86.0	223	4	Q85YK5
2	615	67.4	278	6	Q8SQ34
3	588	62.2	274	6	Q7YRL5
4	563	61.7	277	6	Q8WMQ2
5	477	52.2	289	11	Q8K2X6
6	463	50.7	169	11	Q9JKE0
7	296	32.4	276	13	Q9DD22
8	229.5	25.1	275	11	Q80WM9
9	196.5	21.5	283	6	Q9XSZ8
10	180	19.7	146	13	Q800K7
11	180	19.7	146	13	Q7ZZY4
12	180	19.7	150	11	Q9R230
13	176.5	19.3	462	13	Q805B0
14	174.5	19.1	459	11	Q62327
15	170.5	18.7	328	6	Q9BDP0
16	170	18.6	349	12	O57111

17	170	18.6	349	12	O57110
18	170	18.6	349	12	Q80SR3
19	169	18.5	348	12	O57108
20	169	18.5	348	12	O57277
21	169	18.5	348	12	O57103
22	169	18.5	349	12	O57101
23	168.5	18.5	263	6	Q9XS60
24	168.5	18.5	319	6	Q9TV79
25	168.5	18.5	320	6	Q9XS29
26	168	18.4	331	6	Q9GK36
27	168	18.4	349	12	O57098
28	168	18.4	349	12	O57284
29	167.5	18.3	348	12	O57112
30	167	18.3	318	13	Q7TZH3
31	166	18.2	331	6	Q9BDN0
32	166	18.2	331	6	Q9BDN4
33	166	18.2	331	6	Q9T5N4
34	166	18.2	349	12	O57100
35	166	18.2	349	12	O57102
36	166	18.2	349	12	O57291
37	165	18.1	474	11	Q80W16
38	164	18.0	333	6	Q9BDP2
39	164	18.0	349	12	O57099
40	163.5	17.9	482	11	O88734
41	162.5	17.8	314	6	Q861W6
42	162.5	17.8	334	6	Q9GL40
43	162	17.7	349	12	O57109
44	162	17.7	349	12	O57097
45	162	17.7	349	12	O57305

ALIGNMENTS

RESULT 1  
Q86YK5 PRELIMINARY; PRT; 223 AA.  
ID O86YK5  
AC O86YK5  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE -Tumor necrosis factor receptor superfamily member 5 (Fragment).  
GN TNFRSF5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA He X., Xu L., Zeng Y.;  
RT "Transcripts of CD40 isoform in peripheral mononuclear cells.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY225405; AAC43990.1; -  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.  
DR GO: GO:0005488; F:binding; IEA.  
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO: GO:0006915; P:apoptosis; IEA.  
DR GO: GO:0006955; P:immune response; IEA.  
DR GO: GO:0007155; P:signal transduction; IEA.  
DR GO: GO:0006810; P:transport; IEA.  
DR InterPro: IPR006209; EGF\_like.  
DR InterPro: IPR008063; Fas\_receptor.  
DR InterPro: IPR001993; Mitoch\_carrier.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 4.  
DR PRINTS: PR01680; FASRECEPTOR.  
DR SMART: SM00208; TNFR; 4.  
DR PROSITE: PS01186; EGF\_2; 1.  
DR PROSITE: PS00215; MITOCH\_CARRIER; 1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
DR Receptor.

```
FT NON TER 223 223
SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 86.0%; Score 785; DB 4; Length 223;
Best Local Similarity 95.1%; Pred. No. 1.3e-81;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSLQCPGQKLVSDCTEFTETEC 60
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSLQCPGQKLVSDCTEFTETEC 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
QY 121 LHRSCSPGFGVKQIAPKPTWLC 143
DB 121 LHRSCSPGFGVKQIATGVSDTIC 143

RESULT 2
Q8SQ34 PRELIMINARY; PRT; 278 AA.
AC Q8SQ34;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CD40.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RT "Characterization of the Porcine CD40 Molecule.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248545; AAL92924.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 4.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
SQ SEQUENCE 278 AA; 30951 MW; 20D446BA4AF93DD2 CRC64;

Query Match 67.4%; Score 615; DB 6; Length 278;
Best Local Similarity 71.3%; Pred. No. 4.6e-62;
Matches 102; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSLQCPGQKLVSDCTEFTETEC 60
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYPTNSRCCNLCPPGQKLVNHCTEVTETEC 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
DB 61 PCSSEFLATWNRKCHQHKYCDPNLGLRVQREGTSKDTTTCVSGHCTNSACESCT 120
QY 121 LHRSCSPGFGVKQIAPKPTWLC 143
DB 121 LHLCLPPLGLVKQKQATEVSDTIC 143

RESULT 3
Q7YRL5 PRELIMINARY; PRT; 274 AA.
ID Q7YRL5
AC Q7YRL5;
QY 121 LHLCLPPLGLVKQKQATEVSDTIC 143
```

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD40.
GN CD40.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Sim G.-K.;
RT "Canine CD40 and CD40 Ligand cDNA Sequences.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333789; AAP86653.1; -.
SQ SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;

Query Match 62.2%; Score 568; DB 6; Length 274;
Best Local Similarity 65.3%; Pred. No. 1.1e-56;
Matches 94; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSLQCPGQKLVSDCTEFTETEC 60
DB 1 MVLPLKCLFWGSLTITVPEPTACREKQYLVDSQCCNMCPGKLVNCLHTIDTECT 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
DB 61 RCQTGEFLDTWNAERHCHQHKYCDPNLGLHVEKGTSETDTTCTCDSGLCTNAACESCT 120
QY 121 LHRSCSPGFGVKQIAPKPTWLCN 144
DB 121 MHSICPPGLGVKQIATGISTIDC 144

RESULT 4
Q8WNQ2 PRELIMINARY; PRT; 277 AA.
ID Q8WNQ2
AC Q8WNQ2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Membrane protein CD40 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Zawitkowski M.S., Russ G.R., Krishnan R.;
RT "Cloning and expression of the ovine CD40 molecule and the inhibition of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion protein.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072798; AAL68402.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
FT NON TER 277
SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

Query Match 61.7%; Score 563; DB 6; Length 277;
Best Local Similarity 65.7%; Pred. No. 4e-56;
Matches 94; Conservative 15; Mismatches 34; Indels 0; Gaps 0;
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QY 1 MVRPLQCVLWGLLTAVHPPEPTACREKQYLINSQCCSLQPGQKLVSDCTETETECL 60
Db 1 MVRPLQCVLWGLLTAVHPPEPTACREKQYLINSQCCSLQPGQKLVSDCTETETECL 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEEGWHCTSEACSCV 120
Db 61 SCGGEGFSTWNRREKYECHRYCNPLGLRQSEGLNTDTTCVDEGQHTSHTCSCT 120
QY 121 LHRSCSPGFVGKQIAVRPKTWLC 143
Db 121 PHSLLCLPGFGVKQIATGVLDITC 143

RESULT 5
Q8K2X6 PRELIMINARY; PRT; 289 AA.
AC Q8K2X6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029254; AAH29254.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007155; P:signal transduction; IEA.
DR InterPro; IPR008063; FAS_receptor.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 289 AA; 32077 MW; DBE93BLE439F1E2A CRC64;

Query Match 52.2%; Score 477; DB 11; Length 289;
Best Local Similarity 54.2%; Pred. No. 2.9e-46;
Matches 78; Conservative 21; Mismatches 45; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGLLTAVHPPEPTACREKQYLINSQCCSLQPGQKLVSDCTETETECL 60
Db 1 MVRPLQCVLWGLLTAVHPPEPTACREKQYLINSQCCSLQPGQKLVSDCTETETECL 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEEGWHCTSEACSCV 120
Db 61 PCDSGFSQWNRREIRCHQHRCEPQGLRVKKEGTAESDTCACKEGHCTSKDCEACA 120
QY 121 LHRSCSPGFVGKQIAVRPKTWLCN 144
Db 121 QHTPCIPGFGVMEMATEETDTTVCH 144

RESULT 6
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Q9JKE0 PRELIMINARY; PRT; 169 AA.
AC Q9JKE0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE CD40 protein (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE OF 62-169 FROM N.A.
RA STRAIN=Wistar; TISSUE=Smooth muscle;
RX MEDLINE=9330195; Pubmed=10403401;
RA Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
RT "Cytokine-inducible CD40 gene expression in vascular smooth muscle
RT cells is mediated by nuclear factor kappaB and signal transducer and
RL FBBS Lett. 453:191-196(1999).
RN [2]_
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Smooth muscle;
RX Krzesz R., Hecker M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]_
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Smooth muscle;
RX Gao D., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241231; AAF43717.2; -
DR HSSP; Q92956; IJMA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007155; P:signal transduction; IEA.
DR InterPro; IPR008063; FAS_receptor.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
DR NON TER 169
SQ SEQUENCE 169 AA; 18525 MW; F199D91EFA224A26 CRC64;

Query Match 50.7%; Score 463; DB 11; Length 169;
Best Local Similarity 53.1%; Pred. No. 6.5e-45;
Matches 76; Conservative 21; Mismatches 46; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGLLTAVHPPEPTACREKQYLINSQCCSLQPGQKLVSDCTETETECL 60
Db 1 MLPLPQLCALWGLLTAVHLGQCVCSDKQYLOGGECCLQPGNRLVSHCTALEKTQCQ 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEEGWHCTSEACSCV 120
Db 61 PCDSGFSQWNRREIRCHQHRCEPQGLRVKKEGTAESDTCACKEGHCTSKDCEACA 120
QY 121 LHRSCSPGFVGKQIAVRPKTWLC 143
Db 121 QHRPCGFGVGVMQVATETDTVC 143

RESULT 7
Q9DDD2 PRELIMINARY; PRT; 276 AA.
ID Q9DDD2
```

AC Q9DDD2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Human CD40-homologue.  
 GN TNFSF5.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tregaskes C.A.;  
 RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.  
 DR EMBL; AJ293700; CAC20218.1; -;  
 DR HSP; Q92956; IJMA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR001005; Myb DNA binding.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00037; MYB.1; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

Query Match 32.4%; Score 296; DB 13; Length 276;  
 Best Local Similarity 37.7%; Pred. No. 1.3e-25;  
 Matches 49; Conservative 25; Mismatches 56; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCLQCPQKLVSDCTETETECLE 60  
 DB 1 MGRLLGLLICALLCGCGDVAWSCKQYKHGRCRCQPKLAECDNEDTSVCT 60  
 QY 61 PQSESEFLDWNRETHCHQHYCDPNLGRVQKGTSETDTICTCEGWHCTSE--ACSSVLHRS 120  
 DB 61 PCENGQYQHSWTKRHTCTPCEICEDNAGLIVKRGHGNATHVTQCRCAGMHCSDASQTCV 120  
 QY 121 LHRSCSPGFG 130  
 DB 121 ENFPCKQGGF 130

RESULT 8  
 Q8QW9 ID Q8QW9 PRELIMINARY; PRT; 275 AA.  
 AC Q8QW9  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 14 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6; TISSUE=Thymus;  
 RC Benencia F.; Conejo-Garcia J.R.; Courreges M.C.; Coukos G.;  
 RT "Light regulation in a murine model of ovarian carcinoma."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY264405; AA089081.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR008063; Fas receptor.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SMO0208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Signal.  
 FT SIGNAL 1 38 Potential.  
 SQ SEQUENCE 275 AA; 30171 MW; C4A7EAD8EFC0521D CRC64;

Query Match 25.1%; Score 229.5; DB 11; Length 275;  
 Best Local Similarity 30.9%; Pred. No. 5.4e-18;  
 Matches 43; Conservative 29; Mismatches 62; Indels 5; Gaps 2;

QY 8 CVLWGCLLTAVHPPTACREKQYLINSQCCLQCPQKLVSDCTETETECLEPCGESEF 67  
 DB 26 CVFLNLLQRIASQP--SCQEEFLVGDCCPMCPNPGYHKVQVSEHTGIVCAPCPPTQY 83  
 QY 68 LDTWNRETHCHQHYCDPNLGRVQKGTSETDTICTCEGWHCTSE---ACSSVLHRS 124  
 DB 84 TAHANGLSKCLPCGVCDDPDMGLLTWQECSSWKDVCRCIPGYFCENQDGHSCSTCLOHTT 143  
 QY 125 CSPGPGVKQIAVRPKTWLC 143  
 DB 144 CPGQVRKRGTHDQDVC 162

RESULT 9  
 Q9XSZ8 ID Q9XSZ8 PRELIMINARY; PRT; 283 AA.  
 AC Q9XSZ8  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE HVEAs.  
 GN HVEAs.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=95296730; PubMed=10366573;  
 RA Foster T.P.; Chouljenko V.N.; Kousoulas K.G.;  
 RT "Functional characterization of the HveA homolog specified by African  
 RT green monkey kidney cells with a herpes simplex virus expressing the  
 RT green fluorescence protein.";  
 RL Virology 258:365-374(1999).  
 DR EMBL; AF147720; AAD37381.1; -;  
 DR HSP; Q92956; IJMA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR008063; Fas receptor.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match 21.5%; Score 196.5; DB 6; Length 283;  
 Best Local Similarity 30.3%; Pred. No. 3.3e-14;  
 Matches 37; Conservative 24; Mismatches 58; Indels 3; Gaps 1;

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QY 25 ACREKQYLINCCSLCPGQKLVSDCTFTETECCLPGSESEFLDTWNRETHCHQKXCD 84
DB 41 SCKDEYVPGSCCKPGFHVROACGEQGTVCPCSPGTYYAHFNGLSKCLQCCQNC 100
QY 85 PNLGLRVQKGTSETDTICTCEGWHC---TSEACESCVLHRSCLPGFQVQKIAVRPKTW 141
DB 101 PANGRLTSENCTTANALCGSPGHFCILQGDGHCAACRAVATSSPGQVQKGTESQDT 160
QY 142 LC 143
DB 161 LC 162

RESULT 10
Q800K7 PRELIMINARY; PRT; 483 AA.
AC Q800K7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-2.
GN TNFR_2.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C., Kurobe T., Hirano I., Aoki T.;
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis
RT factor receptor superfamily genes from Japanese flounder Paralicthys
RT olivaceus."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080947; BAC65226.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR Receptor.
KW Receptor.
SQ SEQUENCE 483 AA; 5227 MW; EE55874A8C7F2085 CRC64;

Query Match 21.5%; Score 196.5; DB 13; Length 483;
Best Local Similarity 30.6%; Pred. No. 5.7e-14;
Matches 41; Conservative 19; Mismatches 65; Indels 9; Gaps 3;

QY 4 LPLQCVLWGLLTAVHPBPPTACREK--QYLINSCCLCPGQKLVSDCTFTETECCLP 61
DB 8 LULLCVR---TTAYRLSDSGKHNSTTEYREQLDCKCKCPGQRLIQKSDATESVCKQ 64
QY 62 CGSESEFLDTWNRETHCHQKHYCDPNLGLRVQKGTSETDTICTCEGWHCTSE---ACE 117
DB 65 CDSGQKWEKNVAAQKCLCNKCKSNKGLQYAGRCSSFTITGVCVCKPGNVCINDFNPYCA 124
QY 118 SCVLHRSCLSPFGV 131
DB 125 ECRNYSQCRAGYGV 138

RESULT 11
Q72ZY4 PRELIMINARY; PRT; 146 AA.
AC Q72ZY4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Osteoprotegerin (Fragment).
GN OPG.
OS Gallus gallus (Chicken).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Osteoprotegerin (OPG) expression in the hen ovary."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251407; AAP03890.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
FT NON TER 146
SQ SEQUENCE 146 AA; 16487 MW; 1C9B64FE3A0FC2DF CRC64;

Query Match 19.7%; Score 180; DB 13; Length 146;
Best Local Similarity 30.5%; Pred. No. 1.3e-12;
Matches 39; Conservative 19; Mismatches 54; Indels 16; Gaps 5;

QY 18 VHPBPPTACREKQYLINSCCLCPGQKLVSDCTFTETECCLPGSESEFLDTWNRETHC 77
DB 29 LHVDPGTS---RQVM-----CNQPPGYSYVKQHCCTAASPTVCAPCPDQYVAEDWNSDEC 80
QY 78 HQHKYCDPNLG--LRVQKGTSETDTICTCEGWHCTSEACESCVLHRSCLPGFQVQKIA 135
DB 81 --QYCAVCKELQYIKQCTSTQDRVCECIEGNYL---ELEFLKHKTECPGFGVAQPG 134
QY 136 VRPKTWC 143
DB 135 TPESDTVC 142

RESULT 12
Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fas receptor (Fragment).
OS Rattus norvegicus [rat].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Corpus luteum;
RA Lareu R.R., Dharmarajan A.;
RT "Cloning and expression of Fas and Fas Ligand in the apoptotic rat
RT corpus luteum."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104034; AAD20221.1; -.
DR HSSP; Q92956; LUNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON TER 1

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FT NON TER 150 150
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;

Query Match 19.7%; Score 180; DB 11; Length 150;
Best Local Similarity 33.6%; Pred.No. 1.3e-12;
Matches 36; Conservative 14; Mismatches 55; Indels 2; Gaps 2;

QY 21 EPTACREKQYLNSQCSCSLQCPQKLVSDC-TEFTETELPCGE-SEFLDTWNRTHCH 78
DB 34 ETDNNCEGLYQVGFCCQPCQPCQGERKVKDCTTSGGAPTCHPTCEGEBY'DRXHYSKCR 93
QY 79 QHKYCDNGLRVQKGTSETDTICTCEGWHCTSEACESCVLHRSC 125
DB 94 RCAFCDHGHELVETNCTRTONTKCRCKENFYCNASLCDHCYHCTSC 140

RESULT 13
Q805B0 PRELIMINARY; PRT; 462 AA.
AC Q805B0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-II.
GN TNFR-II.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayde A.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayed A., Horuchi H., Furusawa S., Matsuda H.;
RT "Molecular cloning and characterization of chicken Tumor necrosis
RT factor receptor-II (TNFR-II) and tumor necrosis factor receptor
RT associated factor-5 (TRAF-5) genes.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB101004; BAC55966.1;
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004888; F-transmembrane receptor activity; IEA.
DR GO; GO:0006955; P-immune response; IEA.
DR GO; GO:0007165; P-signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 462 AA; 50141 MW; 8B00A93305414782 CRC64;

Query Match 19.3%; Score 176.5; DB 13; Length 462;
Best Local Similarity 30.8%; Pred.No. 1e-11;
Matches 36; Conservative 16; Mismatches 54; Indels 11; Gaps 4;

QY 22 PPTACREKQYLNSQCSCSLQCPQKLVSDC-TEFTETELPCGESEFLDTWNRTHCHQHK 91
DB 34 PSTEFYEERL---KKCCSKCPGQRKAESCSHSDTKICPLDPTVTAVNRSPOCFA-- 88
QY 82 YCDP--NLGLRVQKGTSETDTICTCEGWHCTSC---EACESCVLHRSCSPGFGYKQ 133
DB 89 -CSPPCKKGFVENQCTLSWDRCISCPNPEYICISKMYQNCHICKVHKCKGRGVRVS 144

RESULT 14
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Q62327
ID Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Murine tumour necrosis factor receptor 2 protein (fragment).
GN TNFRSF1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1;
DR PIR; I48854; I48854.
DR HSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008220; P:necrosis; IMP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER 1 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 19.1%; Score 174.5; DB 11; Length 459;
Best Local Similarity 29.9%; Pred.No. 1.8e-11;
Matches 41; Conservative 20; Mismatches 59; Indels 17; Gaps 6;

QY 4 LPLQVLWGCLLTAVHREPPPTACREKQYLIN---SQCCSLQCPQKLVSDCTETETEC 60
DB 8 VPAQV-----LTPYKPEPGVEYEQISQEYDRKAMCCAKCPGQYVHKFCNKTSDTVCA 62
QY 61 PCGESEFLDTWNRTHCHQHKYCDNGLR-RVQKGT-SETDTICTCEGWHCT-----SE 114
DB 63 DCEASMYTQVWNPRTCLS---CSSSCSTQVETRACTKQNRVCAACEAGRYCAKXTHSG 119
QY 115 ACESCVLHRSCSPGFGV 131
DB 120 SCRCMLSLKCGPGFGV 136

RESULT 15
Q9BDP0 PRELIMINARY; PRT; 328 AA.
ID Q9BDP0
AC Q9BDP0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FAS antigen CD95.
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OS Aotus trivirgatus (Night monkey) (Douroucoulis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotidae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344835; AAK37531.1; -
DR HSSP; P25445; 1DDF
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
FT VARIANT 157 157 S -> T.
SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;

Query Match      18.7%; Score 170.5; DB 6; Length 328;
Best Local Similarity 32.4%; Pred. No. 3, 6e-11;
Matches 36; Conservative 18; Mismatches 54; Indels 3; Gaps 3;

QY 28 EKQYLINSQCCSLQPGQKLVSDCT-EFTETCLPCGE-SBFLDTWNRETHCHQHKYCDP 85
Db 49 EDQYVVGQFCHKPCSPGKPKARDCTVDGDEPCVPCQEGKEYTDKSHFSPKRCRCRLCDE 108
QY 86 NLGLVQOKGTSETTICTCEGWHCTSEACESCVLHSCSPGFGVKQIAV 136
Db 109 GHGLEVINCTNTQNKRCRKNFFCN SAVCEHCDPCTICEHGI-IRKCSL 159

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Job time : 40 secs

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OS Homo sapiens.
XX WO2000066155-A1.
XX PD 09-NOV-2000.
XX PF 28-APR-2000; 2000WO-US011734.
XX PR 30-APR-1999; 99US-0131730P.
XX PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
XX PI Sarawar SR, Schoenberger SP;
XX XX WPI; 2001-024740/03.
XX PT Method for preventing latent virus reactivation or controlling virus
PT replication by administration of antibodies or similar reagents which
PT stimulate the CD40 molecule.
XX PS Disclosure; Page 18; 36pp; English.
XX CC The present sequence is human CD40. It may be used in a method for
CC preventing latent virus reactivation or controlling virus replication.
CC The method comprises administering a composition capable of binding to a
CC cell membrane expressed CD40, where the binding of the composition to the
CC CD40 on the surface of the cell generates a stimulatory signal to the
CC cell. The method is useful for treating immunocompromised patients, e.g.
CC infected with human immunodeficiency virus (HIV), or immunosuppressed
CC patients, e.g. due to infections or illness, or as a side effect of
CC treatments (such as radiation or cancer therapy), or due to tissue or
CC organ transplantation. The method does not have the levels of toxicity
CC seen following administration of conventional antiviral drugs
XX SQ Sequence 277 AA;
Query Match 86.0%; Score 785; DB 4; Length 277;
Best Local Similarity 95.1%; Pred. No. 4e-58;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCPQKLVSDCTETETEC 60
Db 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCPQKLVSDCTETETEC 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
Db 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
QY 121 LHRSCSPGFGVKQIATVPTWLC 143
Db 121 LHRSCSPGFGVKQIATVPTWLC 143
RESULT 15
AAB50520
ID AAB50520 standard; protein; 277 AA.
XX AAB50520;
XX AC
XX DT 15-MAR-2001 (first entry)
XX DE Human tumour necrosis factor receptor CD40 protein SEQ ID NO:10.
XX KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neurotropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX OS Homo sapiens.
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XX FN WO2000071150-A1.
XX PD 30-NOV-2000.
XX PF 18-MAY-2000; 2000WO-US013515.
XX PR 20-MAY-1999; 99US-0135164P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Wei Y, Ruben SM, Gentz RL, Ni J;
XX XX WPI; 2001-041051/05.
XX PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection.
XX PS Disclosure; Fig 2; 285pp; English.
XX CC The present invention describes the human TRID protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor receptor
CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, neurotropic,
CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities, and can be used in gene therapy. The TRID polynucleotides are
CC useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)
CC autoimmune disorders; (c) diseases associated with increased apoptosis;
CC (d) cardiovascular disorders; and (e) viral infection. The present
CC sequence represents a tumour necrosis factor receptor used in comparison
CC with TRID in the exemplification of the present invention
XX SQ Sequence 277 AA;
Query Match 86.0%; Score 785; DB 4; Length 277;
Best Local Similarity 95.1%; Pred. No. 4e-58;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCPQKLVSDCTETETEC 60
Db 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCPQKLVSDCTETETEC 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
Db 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
QY 121 LHRSCSPGFGVKQIATVPTWLC 143
Db 121 LHRSCSPGFGVKQIATVPTWLC 143
```

Search completed: July 21, 2004, 10:05:36  
Job time : 56 secs

KW nucleotide sequence-based technology; antisense drug discovery.

XX Homo sapiens.  
 OS WO9953101-A1.  
 PN 21-OCT-1999.  
 PD  
 XX  
 XX 13-APR-1999; 99WO-US008268.  
 XX 13-APR-1998; 98US-0081483P.  
 PR 28-APR-1998; 98US-00067638.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 PI Cowsett LM, Baker BF, Mcneil J, Freier SM, Sasnor HM, Brooks DG;  
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;  
 XX WPI: 1999-620446/53.  
 DR N-PSDB; AAZ40936.  
 XX  
 XX Identifying compounds which modulate expression of nucleic acids, used to  
 PT provide compounds having defined physical, chemical or bioactive  
 PT properties, e.g. antisense activity.  
 XX  
 PS Example 1; Page 177-179; 264pp; English.  
 XX

CC A method has been developed of defining a set of compounds that modulate  
 CC the expression of a target nucleic acid (tNA) sequence via binding of the  
 CC compounds with the tNA sequence. The method comprises generating a  
 CC library of virtual compounds in silico according to defined criteria, and  
 CC evaluating in silico the binding of the virtual compounds with the tNA  
 CC according to defined criteria. Also described are: (1) a method of  
 CC defining a set of oligonucleotides (ONS) that modulate the expression of  
 CC a tNA sequence via binding of the ONS with the tNA sequence comprising  
 CC generating a library of virtual compounds in silico according to defined  
 CC criteria, and evaluating in silico the binding of the virtual ONS with  
 CC the tNA according to defined criteria; and (2) a method of defining a set  
 CC of compounds that modulate the expression of a tNA sequence via binding  
 CC of the compounds with the tNA. The methods can be used for the generation  
 CC and identification of synthetic compounds having defined physical,  
 CC chemical or bioactive properties. Information gathered from assays of  
 CC such compounds is used to identify nucleic acid sequences that are  
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.  
 CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and  
 CC AAV52701 to AAV52706, represent sequences used in the exemplification of  
 CC the present invention  
 XX

SQ Sequence 277 AA;

Query Match 86.0%; Score 785; DB 2; Length 277;  
 Best Local Similarity 95.1%; Pred. No. 4e-58;  
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETEC 60  
 DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETEC 60  
 QY 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
 DB 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
 QY 121 LHRSCSPGFGVKQIATGVS DTC 143  
 DB 121 LHRSCSPGFGVKQIATGVS DTC 143

RESULT 13

AAB84892  
 ID AAB84892 standard; protein; 277 AA.

XX  
 AC AAB84892;

XX

DT 03-AUG-2001 (first entry)

XX Human CD40 antigen.  
 XX  
 KW Human; CD40; immunosuppressive; B cell; autoimmune disease;  
 KW cell-mediated disease; antibody-mediated disease.  
 XX

OS Homo sapiens.

PN WO200130974-A2.

PD 03-MAY-2001.

PF 25-OCT-2000; 2000WO-US041532.

PR 25-OCT-1999; 99US-0161281P.

PA (TANO-) TANOX INC.

PI Chang N;

XX WPI: 2001-308629/32.

XX Novel CD40-binding non-antibody molecule, that do not cause  
 PT proliferation, differentiation or activation of CD40-expressing cells but  
 PT which inhibit CD40 ligand-induced activation, used to treat autoimmune  
 PT disease.  
 XX

XX Disclosure; Page 18-19; 19pp; English.

XX The present invention relates to non-antibody molecules which bind to an  
 CC epitope on CD40 antigen and do not activate CD40-expressing cells, but  
 CC inhibit CD40-ligand (CD40L) induced activation, and which do not  
 CC interfere with the binding of CD40L to CD40. The present sequence is  
 CC human CD40 antigen. CD40 is a 50 kDa type 1 membrane glycoprotein  
 CC expressed on a variety of cells, including B cells. CD40 is critical for  
 CC B cell function. The non-antibody molecules of the present invention are  
 CC useful for treating autoimmune, cell-mediated and antibody-mediated  
 CC diseases, and conditions in which immunogenic proteins are used  
 CC therapeutically  
 XX

SQ Sequence 277 AA;

Query Match 86.0%; Score 785; DB 4; Length 277;  
 Best Local Similarity 95.1%; Pred. No. 4e-58;  
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETEC 60  
 DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETEC 60  
 QY 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
 DB 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
 QY 121 LHRSCSPGFGVKQIATGVS DTC 143  
 DB 121 LHRSCSPGFGVKQIATGVS DTC 143

RESULT 14

AAB37807  
 ID AAB37807 standard; protein; 277 AA.

XX  
 AC AAB37807;

XX 23-FEB-2001 (first entry)

XX Human CD40.

XX Human; CD40; antiviral; anti-HIV; CD40 stimulant;  
 KW human immunodeficiency virus; HIV; cancer; organ transplantation.

XX

XX 20-NOV-2003 (first entry)  
XX CD40 splice variant protein #SEQ ID 2.  
XX CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;  
XX inflammatory disease; cancer; atherosclerosis; acute injury.  
XX Homo sapiens.  
XX WO2003070768-A2.  
XX 28-AUG-2003.  
XX 24-FEB-2003; 2003WO-IB000665.  
XX 22-FEB-2002; 2002US-0358877P.  
XX (COMP-) COMPUGEN LTD.  
XX Bernstein J, Mintz L, Eshel D;  
XX WPI; 2003-697601/66.  
XX N-PSDB; ADA25629.  
XX Protein, useful for preparing a composition for modulating CD40-CD154  
XX interactions in an individual for treating chronic inflammatory disease,  
XX cancer, atherosclerosis or acute injury.  
XX Claim 1; Page 76-77; 92pp; English.  
XX The invention relates to substantially pure CD40 splice variant proteins  
XX which include tail sequences. Also disclosed is a pharmaceutical  
XX composition comprising the protein and a carrier, an in vitro method of  
XX detecting whether an individual is expressing the protein, and a method  
XX for modulating CD40-CD154 interactions in an individual. The protein of  
XX -the invention is useful for preparing a composition for modulating CD40-  
XX CD154 interactions in an individual for treating chronic inflammatory  
XX disease, cancer, atherosclerosis or acute injury. The current sequence  
XX represents CD40 splice variant protein.  
XX Sequence 244 AA;  
Query Match 86.0%; Score 785; DB 6; Length 244;  
Best Local Similarity 95.1%; Pred. No. 3.6e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCOPGQKLVSDCTFTETECL 60  
Db 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCOPGQKLVSDCTFTETECL 60  
QY 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
Db 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPGFGVKQIAPRPTWLC 143  
Db 121 LHRSCSPGFGVKQIATGVS DTC 143  
RESULT 11  
AAV33499  
ID AAV33499 standard; protein; 276 AA.  
XX AAV33499;  
XX 19-JAN-2000 (first entry)  
XX Human CD40 protein.  
XX Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;  
XX huntingtin polypeptide; Machado-Joseph disease; SCAL; SCA2; SCA6;  
XX atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;

KW Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;  
KW dentatorubropallidoluysian atrophy; cell proliferation; cell survival;  
KW neoplastic; malignant; autoimmune; fibrotic; CD40.  
XX Homo sapiens.  
XX WO9945944-A1.  
XX 16-SEP-1999.  
XX 11-MAR-1999; 99WO-US005250.  
XX 12-MAR-1998; 98US-00041886.  
XX (BURN-) BURNHAM INST.  
XX Bredeesen DE, Rabizadeh S;  
XX WPI; 1999-561617/47.  
XX N-PSDB; AAZ23432.  
XX New proapoptotic dependence peptides, used to develop products for  
XX treating, e.g. Alzheimer's disease.  
XX Disclosure; Page 170-171; 199pp; English.  
XX This invention describes novel pure proapoptotic dependence peptides  
XX which comprise a sequence of an active dependence domain selected from  
XX dependence polypeptides consisting of p75NTR, androgen receptor, DCC,  
XX huntingtin polypeptide, Machado-Joseph disease gene product, SCAL, SCA2,  
XX SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable of  
XX inducing cell death and can be used to develop products to mediate or  
XX inhibit apoptosis. The methods can be used for reducing the severity of a  
XX proapoptotic dependence domain mediated pathological conditions e.g.  
XX Huntington's disease, Alzheimer's disease, Kennedy's disease, Machado-  
XX spinocerebellar ataxia, dentatorubropallidoluysian atrophy, Machado-  
XX Joseph disease, stroke or head trauma. They can also be used for reducing  
XX the severity of a pathological condition mediated by upregulated cell  
XX proliferation or cell survival e.g. neoplastic, malignant, autoimmune or  
XX fibrotic conditions. This sequence represents the human CD40 polypeptide  
XX described in the method of the invention  
XX Sequence 276 AA;  
Query Match 86.0%; Score 785; DB 2; Length 276;  
Best Local Similarity 95.1%; Pred. No. 4e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCOPGQKLVSDCTFTETECL 60  
Db 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCSLCOPGQKLVSDCTFTETECL 60  
QY 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
Db 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPGFGVKQIAPRPTWLC 143  
Db 121 LHRSCSPGFGVKQIATGVS DTC 143  
RESULT 12  
AAV52701  
ID AAV52701 standard; protein; 277 AA.  
XX AAV52701;  
XX 26-JAN-2000 (first entry)  
XX Human CD40 protein.  
XX Identification; genetic target; gene modulation; human;  
KW antisense oligonucleotide; phosphorothioate; target validation;

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Db      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTFTETEC 60
QY      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
Db      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
QY      121  LHRSCSPGFGVKQIAVRPXTWLC 143
Db      121  LHRSCSPGFGVKQIAVGSDTIC 143

RESULT 8
ADA25636
ID      ADA25636 standard; protein; 229 AA.
XX
AC      ADA25636;
XX
DT      20-NOV-2003 (first entry)
XX
DE      CD40 splice variant protein #SEQ ID 8.
XX
KW      CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
KW      inflammatory disease; cancer; atherosclerosis; acute injury.
XX
OS      Homo sapiens.
XX
PN      WO2003070768-A2.
XX
PD      28-AUG-2003.
XX
PF      24-FEB-2003; 2003WO-IB000665.
XX
PR      22-FEB-2002; 2002US-0358877P.
XX
PA      (COMP-) COMPUGEN LTD.
XX
PI      Bernstein J, Mintz L, Eshel D;
XX
DR      WPI; 2003-697601/66.
XX
DR      N-ESDB; ADA25633.
XX
PT      Protein, useful for preparing a composition for modulating CD40-CD154
PT      interactions in an individual for treating chronic inflammatory disease,
PT      cancer, atherosclerosis or acute injury.
XX
PS      Claim 1; Page 84-85; 92pp; English.
XX
CC      The invention relates to substantially pure CD40 splice variant proteins
CC      which include tail sequences. Also disclosed is a pharmaceutical
CC      composition comprising the protein and a carrier, an in vitro method of
CC      detecting whether an individual is expressing the protein, and a method
CC      for modulating CD40-CD154 interactions in an individual. The protein of
CC      the invention is useful for preparing a composition for modulating CD40-
CC      CD154 interactions in an individual for treating chronic inflammatory
CC      disease, cancer, atherosclerosis or acute injury. The current sequence
CC      represents CD40 splice variant protein.
XX
SQ      Sequence 229 AA;

Query Match      86.0%; Score 785; DB 6; Length 229;
Best Local Similarity 95.1%; Pred. No. 3.3e-58;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTFTETEC 60
Db      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTFTETEC 60
QY      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
Db      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
QY      121  LHRSCSPGFGVKQIAVRPXTWLC 143
Db      121  LHRSCSPGFGVKQIAVGSDTIC 143

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Db      121  LHRSCSPGFGVKQIATGVSDTIC 143

RESULT 9
ADA25634
ID      ADA25634 standard; protein; 237 AA.
XX
AC      ADA25634;
XX
DT      20-NOV-2003 (first entry)
XX
DE      CD40 splice variant protein #SEQ ID 6.
XX
KW      CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
KW      inflammatory disease; cancer; atherosclerosis; acute injury.
XX
OS      Homo sapiens.
XX
PN      WO2003070768-A2.
XX
PD      28-AUG-2003.
XX
PF      24-FEB-2003; 2003WO-IB000665.
XX
PR      22-FEB-2002; 2002US-0358877P.
XX
PA      (COMP-) COMPUGEN LTD.
XX
PI      Bernstein J, Mintz L, Eshel D;
XX
DR      WPI; 2003-697601/66.
XX
DR      N-ESDB; ADA25633.
XX
PT      Protein, useful for preparing a composition for modulating CD40-CD154
PT      interactions in an individual for treating chronic inflammatory disease,
PT      cancer, atherosclerosis or acute injury.
XX
PS      Claim 1; Page 82-83; 92pp; English.
XX
CC      The invention relates to substantially pure CD40 splice variant proteins
CC      which include tail sequences. Also disclosed is a pharmaceutical
CC      composition comprising the protein and a carrier, an in vitro method of
CC      detecting whether an individual is expressing the protein, and a method
CC      for modulating CD40-CD154 interactions in an individual. The protein of
CC      the invention is useful for preparing a composition for modulating CD40-
CC      CD154 interactions in an individual for treating chronic inflammatory
CC      disease, cancer, atherosclerosis or acute injury. The current sequence
CC      represents CD40 splice variant protein.
XX
SQ      Sequence 237 AA;

Query Match      86.0%; Score 785; DB 6; Length 237;
Best Local Similarity 95.1%; Pred. No. 3.4e-58;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTFTETEC 60
Db      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTFTETEC 60
QY      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
Db      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
QY      121  LHRSCSPGFGVKQIAVRPXTWLC 143
Db      121  LHRSCSPGFGVKQIATGVSDTIC 143

RESULT 10
ADA25630
ID      ADA25630 standard; protein; 244 AA.
XX
AC      ADA25630;

```

CC therapy procedures. The current sequence is that of the human CD40 (D1-  
CC D3)-6XHis mutant extracellular domain protein of the invention.

XX  
SQ Sequence 153 AA;

Query Match 86.0%; Score 785; DB 7; Length 153;  
Best Local Similarity 95.1%; Pred. No. 2.2e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACESC 120

DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACESC 120

QY 121 LHRSCSPFGVKGQIAVRPXTWLC 143

DB 121 LHRSCSPFGVKGQIATGVSDTIC 143

#### RESULT 6

ADA25632

ID ADA25632 standard; protein; 191 AA.

XX

AC ADA25632;

XX

DT 20-NOV-2003 (first entry)

DE

DE CD40 splice variant protein #SEQ ID 4.

XX

XX CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;

XX inflammatory disease; cancer; atherosclerosis; acute injury.

OS Homo sapiens.

XX

PN WO2003070768-A2.

XX

PD 28-AUG-2003.

XX

PF 24-FEB-2003; 2003WO-IB000665.

XX

PR 22-FEB-2002; 2002US-0358877P.

XX

PA (COMP-) COMPUGEN LTD.

XX

PI Bernstein J, Mintz L, Eshel D;

XX

DR WPI; 2003-697601/66.

XX

DR N-PSDB; ADA25631.

XX

PT Protein, useful for preparing a composition for modulating CD40-CD154

PT interactions in an individual for treating chronic inflammatory disease,

PT cancer, atherosclerosis or acute injury.

PS Claim 1; Page 79-80; 92pp; English.

XX

CC The invention relates to substantially pure CD40 splice variant proteins

CC which include tail sequences. Also disclosed is a pharmaceutical

CC composition comprising the protein and a carrier, an in vitro method of

CC detecting whether an individual is expressing the protein, and a method

CC for modulating CD40-CD154 interactions in an individual. The protein of

CC the invention is useful for preparing a composition for modulating CD40-

CD154 interactions in an individual for treating chronic inflammatory

disease, cancer, atherosclerosis or acute injury. The current sequence

represents CD40 splice variant protein.

XX

SQ Sequence 191 AA;

Query Match 86.0%; Score 785; DB 6; Length 191;

Best Local Similarity 95.1%; Pred. No. 2.8e-58;

Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACESC 120

DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACESC 120

QY 121 LHRSCSPFGVKGQIAVRPXTWLC 143

DB 121 LHRSCSPFGVKGQIATGVSDTIC 143

RESULT 7

ADA28516

ID ADE28516 standard; protein; 197 AA.

XX

AC ADE28516;

XX

DT 29-JAN-2004 (first entry)

DE

DE Human CD40-6XHis wild-type extracellular domain protein.

XX

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;

XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;

XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;

XX human; wild-type; extracellular domain; CD40-6XHis.

XX Synthetic.

OS Homo sapiens.

XX

PN WO2003040170-A2.

XX

PD 15-MAY-2003.

XX

PF 08-NOV-2002; 2002WO-US036107.

XX

PR 09-NOV-2001; 2001US-0348980P.

XX

PA (PFIZ ) PFIZER PROD INC.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX

XX WPI; 2003-441521/41.

XX

PT New chimeric or human monoclonal antibody or its antigen-binding portion

PT that specifically binds to and activates human CD40, useful for enhancing

PT an immune response in a human, or treating cancer, HIV, neutropenia or

PT viral infections.

XX

PS Example 14; SEQ ID NO 139; 177pp; English.

XX

CC The invention relates to a novel chimeric or human monoclonal antibody or

CC its antigen-binding portion that specifically binds to and activates

CC human CD40. The anti-CD40 antibody of the invention demonstrates

CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

CC activities and may be useful for treating a hyperproliferative disorder

CC such as cancer, viral and bacterial infection or genetic, primary or

CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40

CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human CD40-6XHis

CC wild-type extracellular domain protein of the invention.

XX

SQ Sequence 197 AA;

Query Match 86.0%; Score 785; DB 7; Length 197;

Best Local Similarity 95.1%; Pred. No. 2.9e-58;

Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACESC 120

DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACESC 120

QY 121 LHRSCSPFGVKGQIAVRPXTWLC 143

DB 121 LHRSCSPFGVKGQIATGVSDTIC 143

CC capable of binding to a CD40R variant and affecting the binding affinity  
CC of the variant to a CD40 ligand  
XX  
SQ Sequence 246 AA;  
Query Match 86.3%; Score 787.5; DB 4; Length 246;  
Best Local Similarity 83.0%; Pred. No. 2.2e-58;  
Matches 142; Conservative 5; Mismatches 11; Indels 13; Gaps 2;  
QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLSQPGQKLVSDCTEFTETECL 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLSQPGQKLVSDCTEFTETECL 60  
QY 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
DB 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPFGVGKQIAVRPKTW-----LCNRQAQTRLMLSVVPRI 159  
DB 121 LHRSCSPFGVGKQIACTETDLVVQAGTNKTDVWCGPQDLRALV-VIPII 170  
RESULT 4  
ABR63594  
ID ABR63594 standard; protein; 246 AA.  
XX  
AC ABR63594;  
DT 18-SEP-2003 (first entry)  
XX  
DE Human oxifan protein.  
XX  
KW Metabolic research; oxifan; agonist; antagonist; body mass; obesity;  
KW hyperlipidaemia; atherosclerosis; insulin resistance; diabetes;  
KW hypertension; anorectic; antilipemic; antiarteriosclerotic; antidiabetic;  
KW hypotensive; immunomodulator; anti-HIV; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= signal\_peptide  
FT Domain 21..161  
FT /label= EC\_domain  
FT Domain 162..184  
FT /label= transmembrane\_domain  
FT Domain 185..246  
FT /label= IC\_domain  
XX  
FN WO2003049759-A1.  
XX  
PD 19-JUN-2003.  
XX  
PF 14-OCT-2002; 2002WO-IB004634.  
XX  
PR 13-DEC-2001; 2001US-0340414P.  
XX  
XX (GEST ) GENSET SA.  
XX  
XX Dialynas D, Scallia A;  
XX  
XX WPI; 2003-569079/53.  
XX  
XX N-PSDB; ACC85399.  
XX  
XX New agonist or antagonist of Oxifan activity, useful for preventing or  
XX treating metabolic disorders such as obesity or obesity-related disorders  
XX (e.g. hyperlipidaemia) or those associated with excessive weight loss  
XX (e.g. anorexia).  
XX  
XX Disclosure; Page 33-34; 37pp; English.  
XX  
XX The present invention relates to agonists and antagonists of oxifan, a  
XX member of the tumour necrosis factor receptor superfamily. These can be

CC used in preventing and treating obesity-related diseases, including  
CC hyperlipidaemia, atherosclerosis, insulin resistance, diabetes and  
CC hypertension. The present sequence is the human oxifan protein described  
XX in the invention  
SQ Sequence 246 AA;  
Query Match 86.3%; Score 787.5; DB 6; Length 246;  
Best Local Similarity 83.0%; Pred. No. 2.2e-58;  
Matches 142; Conservative 5; Mismatches 11; Indels 13; Gaps 2;  
QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLSQPGQKLVSDCTEFTETECL 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLSQPGQKLVSDCTEFTETECL 60  
QY 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
DB 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPFGVGKQIAVRPKTW-----LCNRQAQTRLMLSVVPRI 159  
DB 121 LHRSCSPFGVGKQIACTETDLVVQAGTNKTDVWCGPQDLRALV-VIPII 170  
RESULT 5  
ADE28517  
ID ADE28517 standard; protein; 153 AA.  
XX  
AC ADE28517;  
DT 29-JAN-2004 (first entry)  
XX  
DE Human CD40 (D1-D3)-6XHis mutant extracellular domain protein.  
XX  
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; mutant; mutein; extracellular domain; (D1-D3)-6XHis.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FN WO2003040170-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 08-NOV-2002; 2002WO-US036107.  
XX  
PR 09-NOV-2001; 2001US-0348980P.  
XX  
XX (PFIZ ) PFIZER PROD INC.  
XX (ABGE-) ABGENIX INC.  
XX  
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX  
XX WPI; 2003-441521/41.  
XX  
XX New chimeric or human monoclonal antibody or its antigen-binding portion  
XX that specifically binds to and activates human CD40, useful for enhancing  
XX an immune response in a human, or treating cancer, HIV, neutropenia or  
XX viral infections.  
XX  
XX Example 14; SEQ ID NO 140; 177pp; English.  
XX  
XX The invention relates to a novel chimeric or human monoclonal antibody or  
XX its antigen-binding portion that specifically binds to and activates  
XX human CD40. The anti-CD40 antibody of the invention demonstrates  
XX cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
XX activities and may be useful for treating a hyperproliferative disorder  
XX such as cancer, viral and bacterial infection or genetic, primary or  
XX combined immunodeficiency conditions including neutropenia or HIV  
XX infection. The anti-CD40 antibodies may also be useful for detecting CD40  
XX in a biological sample in vitro or in vivo, as well as during gene

CC e.g. rheumatoid arthritis, systemic lupus erythematosus, and multiple  
CC sclerosis, inflammatory diseases and graft versus host disease. Also  
CC claimed are methods for detecting the presence of a variant CD40R in a  
CC sample, for determining the level of variant CD40R in a sample, and for  
CC determining the ratio between the level of a CD40R variant acid and the  
CC level of original CD40R, and a method for identifying candidate compounds  
CC capable of binding to a CD40R variant and affecting the binding affinity  
CC of the variant to a CD40 ligand  
XX

SQ Sequence 160 AA;

Query Match 100.0%; Score 913; DB 4; Length 160;  
Best Local Similarity 100.0%; Pred. NO. 4e-69;  
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETECCL 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETECCL 60  
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBEGWHCTSEACSCV 120  
DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBEGWHCTSEACSCV 120  
QY 121 LHRSCSPGFGVKQIAVRPKTWLCNRQAOTRLMLSVVPRIG 160  
DB 121 LHRSCSPGFGVKQIAVRPKTWLCNRQAOTRLMLSVVPRIG 160

RESULT 2

ADA25635  
ID ADA25635 standard; protein; 156 AA.

XX ADA25635;

XX 20-NOV-2003 (first entry)

XX CD40 splice variant protein #SEQ ID 7.

XX CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;  
XX inflammatory disease; cancer; atherosclerosis; acute injury.

XX Homo sapiens.

XX WO2003070768-A2.

XX 28-AUG-2003.

XX 24-FEB-2003; 2003WO-IB000665.

XX 22-FEB-2002; 2002US-0358877P.

XX (COMP-) COMPUGEN LTD.

PI Bernstein J, Mintz L, Eshel D;

XX WPI; 2003-697601/66.

XX Protein, useful for preparing a composition for modulating CD40-CD154  
XX interactions in an individual for treating chronic inflammatory disease,  
XX cancer, atherosclerosis or acute injury.

XX Claim 1; Page 83-84; 92pp; English.

XX The invention relates to substantially pure CD40 splice variant proteins  
XX which include tail sequences. Also disclosed is a pharmaceutical  
XX composition comprising the protein and a carrier, an in vitro method of  
XX detecting whether an individual is expressing the protein, and a method  
XX for modulating CD40-CD154 interactions in an individual. The protein of  
XX the invention is useful for preparing a composition for modulating CD40-  
XX CD154 interactions in an individual for treating chronic inflammatory  
XX disease, cancer, atherosclerosis or acute injury. The current sequence  
XX represents CD40 splice variant protein.

SQ Sequence 156 AA;

Query Match 97.6%; Score 891; DB 6; Length 156;  
Best Local Similarity 100.0%; Pred. NO. 2.8e-67;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETECCL 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETECCL 60  
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBEGWHCTSEACSCV 120  
DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBEGWHCTSEACSCV 120  
QY 121 LHRSCSPGFGVKQIAVRPKTWLCNRQAOTRLMLSVV 156  
DB 121 LHRSCSPGFGVKQIAVRPKTWLCNRQAOTRLMLSVV 156

RESULT 3

AAB20170  
ID AAB20170 standard; protein; 246 AA.

XX AAB20170;

XX 30-APR-2001 (first entry)

XX Human CD40 receptor splice variant.

XX CD40 receptor; CD40R; human; splice variant; antiinflammatory;  
XX immunosuppressive; antiarthritic; antirheumatic; dermatological;  
XX neuroprotective; therapy; diagnosis.

XX Homo sapiens.

XX WO200105967-A1.

XX 25-JAN-2001.

XX 19-JUL-2000; 2000WO-IL000427.

XX 20-JUL-1999; 99IL-00130989.

XX (COMP-) COMPUGEN LTD.

PI Savitzky K, Khosravi R, Elazar M;

XX WPI; 2001-147341/15.

XX N-PSDB; AAF30276.

XX Nucleic acid encoding alternative splicing variant of CD40 receptor,  
XX useful for treating inflammatory diseases, autoimmune diseases, and graft  
XX versus host reaction.

XX Claim 4; Page 62-63; 70pp; English.

XX The present sequence is that of a novel splice variant of the human CD40  
XX receptor (CD40R). The variant has the extracellular domain of the native  
XX protein from the signal peptide up to the amino acid before the  
XX transmembrane region. 6. Novel splice variants (see AAB20169-74) of human  
XX and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
XX expression vectors, host cells and antibodies are claimed. Also claimed  
XX is a pharmaceutical composition consisting of a variant CD40R polypeptide  
XX for treatment of diseases which can be ameliorated, cured or prevented by  
XX either decreasing the level or of at least 1 ligand of CD40R, or by  
XX increasing the level of a CD40R variant; antibodies can be used to reduce  
XX the level of a CD40R variants. The diseases include autoimmune diseases  
XX e.g. rheumatoid arthritis, systemic lupus erythematosus, and multiple  
XX sclerosis, inflammatory diseases and graft versus host disease. Also  
XX claimed are methods for detecting the presence of a variant CD40R in a  
XX sample, for determining the level of variant CD40R in a sample, and for  
XX determining the ratio between the level of a CD40R variant acid and the  
XX level of original CD40R, and a method for identifying candidate compounds

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OM protein - protein search, using sw model

Run on: July 21, 2004, 09:59:29 ; Search time 54 Seconds  
(without alignments)

837.178 Million cell updates/sec

Title: US-10-031-607-7

Perfect score: 913

Sequence: 1 MVRPLQCVLWGCLLTAHP.....WLCNRQAQRLMLSVVPRIG 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	913	100.0	160	4	Aab20169 Human CD4
2	891	97.6	156	6	Ada25635 CD40 spli
3	787.5	86.3	246	4	Aab20170 Human CD4
4	787.5	86.3	246	6	Abr63594 Human oxi
5	785	86.0	153	7	Ada28517 Human CD4
6	785	86.0	191	6	Ada25632 CD40 spli
7	785	86.0	197	7	Ada28516 Human CD4
8	785	86.0	229	6	Ada25636 CD40 spli
9	785	86.0	237	6	Ada25634 CD40 spli
10	785	86.0	244	6	Ada25630 CD40 spli
11	785	86.0	276	2	Aay33499 Human CD4
12	785	86.0	277	2	Aay52701 Human CD4
13	785	86.0	277	4	Aab4892 Human CD4
14	785	86.0	277	4	Aab37807 Human CD4
15	785	86.0	277	4	Aab50520 Human tum
16	785	86.0	277	5	Aae19354 Human CD4
17	785	86.0	277	5	Aao18051 CD40 B-ce
18	785	86.0	277	6	Abr58624 Human can
19	785	86.0	277	6	Abr40010 Human Mox
20	785	86.0	277	6	Abg73061 Human CD4
21	785	86.0	277	6	Ada25652 CD40 wild
22	785	86.0	277	7	Add18920 Human dis
23	780	85.4	281	5	Abp70127 Human NOV
24	779	85.3	225	5	Abp70126 Human NOV
25	778	85.2	237	6	Ada09880 Human rec

## ALIGNMENTS

RESULT 1

AAB20169

ID AAB20169 standard; protein; 160 AA.

XX AC AAB20169;

XX DT 30-APR-2001 (first entry)

XX DE Human CD40 receptor splice variant.

XX KW CD40 receptor; CD40R; human; splice variant; antiinflammatory;

XX KW immunosuppressive; antiarthritic; antirheumatic; dermatological;

XX KW neuroprotective; therapy; diagnosis.

XX OS Homo sapiens.

XX PN WC200105967-A1.

XX PD 25-JAN-2001.

XX PF 19-JUL-2000; 2000WO-IL000427.

XX PR 20-JUL-1999; 99IL-00130989.

XX (COMP-) COMPUGEN LTD.

XX SA Savitzky K, Khosravi R, Elazar M;

XX WPI; 2001-147341/15.

XX N-PSDB; AAF30275.

XX Nucleic acid encoding alternative splicing variant of CD40 receptor,

XX useful for treating inflammatory diseases, autoimmune diseases, and graft

XX versus host reaction.

XX Claim 4; Page 61; 70pp; English.

XX The present sequence is that of a novel splice variant of the human CD40 receptor (CD40R). The variant has the extracellular domain of the native protein from the signal peptide up to the amino acid before the transmembrane region. 6 Novel splice variants (see AAB20169-74) of human and murine CD40R, nucleic acids (see AAF30275-80) encoding them, expression vectors, host cells and antibodies are claimed. Also claimed is a pharmaceutical composition consisting of a variant CD40R polypeptide for treatment of diseases which can be ameliorated, cured or prevented by either decreasing the level or of at least 1 ligand of CD40R, or by increasing the level of a CD40R variant, antibodies can be used to reduce the level of a CD40R variants. The diseases include autoimmune diseases

Ade25748 Human pro  
Aar38859 CD40 prot  
Aay32191 CD40 prot  
Abg22935 Novel hum  
Abp70128 Human NOV  
Ada49703 Extracell  
Aay94713 Tumour ne  
Aay95322 Pig costi  
Ade28518 Human CD4  
Aay58212 Canine CD  
Ada25638 Murine CD  
Aay22934 Novel hum  
Aab20171 Mouse CD4  
Aay58213 Canine ma  
Aab20173 Mouse CD4  
Aab66982 Cd40 prot  
Aab20172 Mouse CD4  
Aay94715 Murine CD  
Aab20174 Mouse CD4  
Aaw94647 TNF-R ext

26 778 85.2 277 7 ADE25748  
27 763 83.6 277 2 AAR38859  
28 760 83.2 277 2 AAY32191  
29 759 83.1 306 4 ABG22935  
30 664 72.7 125 5 ABP70128  
31 648 71.0 163 6 ADA49703  
32 638 69.9 173 3 AAY94713  
33 619 67.8 278 3 AAY95322  
34 611 66.9 111 7 ADE28518  
35 568 62.2 274 3 AAY58212  
36 548 60.0 160 6 ADA25638  
37 532 58.3 839 4 ABG22934  
38 526 57.6 156 4 AAB20171  
39 500 54.8 255 3 AAY58213  
40 483 52.9 195 4 AAB20173  
41 483 52.9 197 4 AAB66982  
42 483 52.9 203 4 AAB20172  
43 483 52.9 281 3 AAY94715  
44 465 50.9 211 4 AAB20174  
45 447 49.0 75 2 AAW94647

Result No.	Score	Query Match	Length	DB	ID	§		Description
						Score	Length	
1	809	100.0	809	4	AAE30280			Aaf30280 Mouse CD4
2	742	91.7	776	4	AAE30278			Aaf30278 Mouse CD4
3	679	83.9	1579	6	ABQ74499			Abq74499 Mouse CD4
4	547	67.6	788	4	AAE30279			Aaf30279 Mouse CD4
5	429.2	53.1	934	4	AAE30277			Aaf30277 Mouse CD4
6	312.8	38.7	469	6	ABQ74500			Abq74500 Mouse CD4
7	280.4	34.7	910	8	ADA25651			Ad25651 CD40 wild
8	280.4	34.7	1004	1	AAE90617			Aan90617 CD40 cDNA
9	280.4	34.7	1004	2	AAE14706			Aan14706 Human CD4
10	280.4	34.7	1004	2	AAE63454			Aav63454 Human CD4
11	280.4	34.7	1004	2	AAE40936			Aaz40936 Human CD4
12	280.4	34.7	1004	2	AAE81198			Aav81198 Human CD4
13	280.4	34.7	1004	2	AAE23432			Aaz23432 Human CD4
14	280.4	34.7	1004	3	AAE50590			Aas50590 Human cel
15	280.4	34.7	1004	3	AAE47769			Aas47769 Human CD4
16	280.4	34.7	1004	4	AAE03184			Aas03184 Human lym
17	280.4	34.7	1004	6	AAE147328			Aal147328 CD40 B-c
18	280.4	34.7	1004	7	ACA56689			ACA56689 Human sig
19	280.4	34.7	1004	7	ACC72771			ACC72771 Human can
20	280.4	34.7	1004	7	ACC00289			ACC00289 Human wor
21	280.4	34.7	1004	7	ABX14593			Abx14593 Human CD4
22	280.4	34.7	1004	9	ADD18921			Add18921 Human dis
23	280.4	34.7	1004	9	ADE85051			Ad85051 Farnesyl

CC amino acids. In addition, there is a 9-amino acid insert at position 86  
CC of the original protein, instead of the original Asn. The variant is  
CC missing part of TNFR Cys repeat 4, the transmembrane domain and the  
CC cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of human  
CC and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
CC expression vectors, host cells and anti-CD40R antibodies are claimed.  
CC Also claimed is a pharmaceutical composition consisting of an expression  
CC vector comprising a CD40R nucleic acid, for treatment of diseases which  
CC can be ameliorated, cured or prevented by either decreasing the level or  
CC of at least 1 ligand of CD40R, by increasing the level of a CD40R  
CC variant, or by reducing the level of a CD40R variant. The diseases  
CC include autoimmune diseases e.g. rheumatoid arthritis, systemic lupus  
CC erythematosus, and multiple sclerosis, inflammatory diseases and graft  
CC versus host disease. Also claimed are methods for detecting the presence  
CC of a variant nucleic acid sequence of CD40R in a sample, for determining  
CC the level of variant nucleic acid sequences of CD40R in a sample, and for  
CC determining the ratio between the level of a CD40R variant nucleic acid  
CC and the level of the original CD40R, e.g. using a nucleic acid chip  
XX  
SQ Sequence 809 BP; 194 A; 213 C; 229 G; 173 T; 0 U; 0 Other;  
Query Match 100.0%; Score 809; DB 4; Length 809;  
Best Local Similarity 100.0%; Pred. No. 4e-249;  
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTGTCTTTCCTCGGCTGTGCGCGCTATGGGCTGCTGTGTGACAGGGTCCATCTA 60  
Db 1 ATGGTGTCTTTCCTCGGCTGTGCGCGCTATGGGCTGCTGTGTGACAGGGTCCATCTA 60  
QY 61 GGGCAGTGTGTACGTGACGTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
Db 61 GGGCAGTGTGTACGTGACGTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
QY 121 TGGCAGCCAGGAAGCCGACTGACAGCCACTGACAGCTCTTGAGAGAGCCCAATGCCAC 180  
Db 121 TGGCAGCCAGGAAGCCGACTGACAGCCACTGACAGCTCTTGAGAGAGCCCAATGCCAC 180  
QY 181 CCATGTGACTCAGCGCAATCTCAGCCAGTGGAAACAGGAGATTCGCTGTCCACGAGCAC 240  
Db 181 CCATGTGACTCAGCGCAATCTCAGCCAGTGGAAACAGGAGATTCGCTGTCCACGAGCAC 240  
QY 241 AGACACTGTGAACCCAGTGGGGTGTGCTGGGAAGGATCAAGGGCTTCGGGTTAAG 300  
Db 241 AGACACTGTGAACCCAGTGGGGTGTGCTGGGAAGGATCAAGGGCTTCGGGTTAAG 300  
QY 301 AAGGAGGSCACCGCAGATCAGACACTGTCTGTACCTGTAGGAGAGACAACTGCACC 360  
Db 301 AAGGAGGSCACCGCAGATCAGACACTGTCTGTACCTGTAGGAGAGACAACTGCACC 360  
QY 361 AGCAAGGATTGCGAGGATGTGCTCAGCACACGCGCTGTATCCCTGGCTTTGGAGTTATG 420  
Db 361 AGCAAGGATTGCGAGGATGTGCTCAGCACACGCGCTGTATCCCTGGCTTTGGAGTTATG 420  
QY 421 GAGATGSCCACTGACACTGATACCGTGTGTATCCCTGCCAGTCGCTTCTCTCC 480  
Db 421 GAGATGSCCACTGACACTGATACCGTGTGTATCCCTGCCAGTCGCTTCTCTCC 480  
QY 481 AATCAGTCACTACATTTTCGAAAAGTGTATCCCTGGCAAGAGTTTAAAGTCCCGGATGCG 540  
Db 481 AATCAGTCACTACATTTTCGAAAAGTGTATCCCTGGCAAGAGTTTAAAGTCCCGGATGCG 540  
QY 541 AGCCCTGCTGTGATCTGCTGTGATGGGATCTCTATCACCATTTCGGGGTGTTCCT 600  
Db 541 AGCCCTGCTGTGATCTGCTGTGATGGGATCTCTATCACCATTTCGGGGTGTTCCT 600  
QY 601 CTATATCAAAAAGTGTCAAGAAACCAAGGATATGAGATGTATCCCTCGGCTCGGCTCG 660  
Db 601 CTATATCAAAAAGTGTCAAGAAACCAAGGATATGAGATGTATCCCTCGGCTCGGCTCG 660  
QY 661 ACGGCAAGATCCCGCAGAGATGGAAGATTATCCGGTCAATACACCGCTCTCCAGTGA 720  
Db 661 ACGGCAAGATCCCGCAGAGATGGAAGATTATCCGGTCAATACACCGCTCTCCAGTGA 720

QY 721 GGAGACACTGCACGGGTGTGAGCCTGTCCACACAGAGGATCGTTAAAGAGATCCCATCTC 780  
Db 721 GGAGACACTGCACGGGTGTGAGCCTGTCCACACAGAGGATCGTTAAAGAGATCCCATCTC 780  
QY 781 AGTGCAGGAGCGGCGAGGTGACAGACAGCA 809  
Db 781 AGTGCAGGAGCGGCGAGGTGACAGACAGCA 809  
RESULT 2  
AAE30278  
ID AAF30278 standard; cDNA; 776 BP.  
XX  
AC AAF30278;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Mouse CD40 receptor splice variant cDNA clone Mcd40Alt8.  
XX  
XX CD40 receptor; CD40R; mouse; splice variant; antiinflammatory;  
KW immunosuppressive; antiarthritic; antirheumatic; dermatological;  
KW neuroprotective; gene therapy; diagnosis; ss.  
XX  
OS Mus musculus.  
XX  
XX  
XX Key Location/Qualifiers  
FT CDS 1..612  
FT /\*tag= a  
XX  
XX WC200105967-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 19-JUL-2000; 2000WO-IL000427.  
XX  
XX 20-JUL-1999; 99IL-00130989.  
XX  
XX (COMP-) COMPUGEN LTD.  
XX  
XX Savitzky K, Khosravi R, Elazar M;  
XX  
XX WPI; 2001-147341/15.  
XX P-PSDB; AAB20172.  
XX  
XX Nucleic acid encoding alternative splicing variant of CD40 receptor,  
PT useful for treating inflammatory diseases, autoimmune diseases, and graft  
PT versus host reaction.  
XX  
XX Claim 1; Page 59-60; 70pp; English.  
XX  
XX The present sequence is that of mouse cDNA encoding splice variant  
XX Mcd40Alt8 (see AAB20172) of the mouse CD40 receptor (CD40R). The variant  
XX contains 165 N-terminal amino acids of the original CD40R sequence  
XX including tumour necrosis factor receptor (TNFR) Cys repeats 1, 2 and 3,  
XX and part of TNFR Cys repeat 4, with 38 alternative C-terminal amino  
XX acids. It is missing part of TNFR repeat 4, the transmembrane domain and  
XX the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of  
XX human and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
XX expression vectors, host cells and anti-CD40R antibodies are claimed.  
XX Also claimed is a pharmaceutical composition consisting of an expression  
XX vector comprising a CD40R nucleic acid, for treatment of diseases which  
XX can be ameliorated, cured or prevented by either decreasing the level or  
XX of at least 1 ligand of CD40R, by increasing the level of a CD40R  
XX variant, or by reducing the level of a CD40R variant. The diseases  
XX include autoimmune diseases e.g. rheumatoid arthritis, systemic lupus  
XX erythematosus, and multiple sclerosis, inflammatory diseases and graft  
XX versus host disease. Also claimed are methods for detecting the presence  
XX of a variant nucleic acid sequence of CD40R in a sample, for determining  
XX the level of variant nucleic acid sequences of CD40R in a sample, and for  
XX determining the ratio between the level of a CD40R variant nucleic acid  
XX and the level of the original CD40R, e.g. using a nucleic acid chip  
XX  
XX Sequence 776 BP; 188 A; 205 C; 213 G; 169 T; 0 U; 0 Other;



```

Db      249 AGACACTGTGAACCCA-----ATCAAGGGCTTCGGGTTAAG 284
Qy      301 AAGGAGGACCGCAGAAATCAGACACTGTCTGTACTGTAAAGGAAGCAACAACCTCCACC 360
DR      |
DR      |
Db      285 AAGGAGGACCGCAGAAATCAGACACTGTCTGTACTGTAAAGGAAGCAACAACCTCCACC 344
Qy      361 AGCAGAGATTGCGAGGATGTCTCAGCACAGCCCTGTATCCCTGCTTGGAGTTATG 420
Db      345 AGCAAGGATTGCGAGGATGTCTCAGCACAGCCCTGTATCCCTGCTTGGAGTTATG 404
Qy      421 GAGATGCCACTGAGACACTGATACCTGTCTCATCCCTGCCAGTCGGCTTCTCTCC 480
Db      405 GAGATGCCACTGAGACCACTGATACCTGTCTCATCCCTGCCAGTCGGCTTCTCTCC 464
Qy      481 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGAGCAA-----520
Db      465 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAAGCTGTGAGGATAAGAACTTG 524
Qy      521 -----GGTTTAAAGTCCCGGATG 538
Db      525 GAGTCTCTACAGAAAGCAAGTCAGACTAATGTCTATCTGTGTTTAAAGTCCCGGATG 584
Qy      539 CGAGCCCTGTGTGTCATCTCTGTGTGATGGGATCTCTATCACTTTTCGGGGTGT 598
Db      585 CGAGCCCTGTGTGTCATCTCTGTGTGATGGGATCTCTATCACTTTTCGGGGTGT 644
Qy      599 CTCCTATATCAAAAGTGTTCAAGAACCAAGGATAATGAGATGTTTACCCCTCGGGCT 658
Db      645 CTCCTATATCAAAAGTGTTCAAGAACCAAGGATAATGAGATGTTTACCCCTCGGGCT 704
Qy      659 CGAGCGCAAGATCCCGAGGAGATGGAAGATTATCCCGTCAATACACCGCTGTCCAGTG 718
Db      705 CGAGCGCAAGATCCCGAGGAGATGGAAGATTATCCCGTCAATACACCGCTGTCCAGTG 764
Qy      719 CAGGAGACACTGCAGGGTGTGACCTGTACACAGGAGGATGGTAAAGAGATCCGATC 778
Db      765 CAGGAGACACTGCAGGGTGTGACCTGTACACAGGAGGATGGTAAAGAGATCCGATC 824
Qy      779 TCAGTGAGGAGCGGAGGTGACAGACAGCA 809
Db      825 TCAGTGAGGAGCGGAGGTGACAGACAGCA 855

RESULT 4
ID AAF30279
XX AAF30279 standard; cDNA; 788 BP.
AC AAF30279;
XX AAF30279;
DT 30-APR-2001 (first entry)
XX
DE Mouse CD40 receptor splice variant cDNA clone Mcd40Alt19.
XX
KW CD40 receptor; CD40R; mouse; splice variant; antiinflammatory;
KW immunosuppressive; antiarthritic; antirheumatic; dermatological;
KW neuroprotective; gene therapy; diagnosis; ss.
XX
OS Mus musculus.
XX
Key Location/Qualifiers
PH 1..588
CDS /*tag= a
FT
XX
XX WO200105967-A1.
XX
XX 25-JAN-2001.
XX
XX 19-JUL-2000; 2000WO-IL000427.
XX
XX 20-JUL-1999; 99IL-00130989.
XX
XX (COMP-) COMPUEN LTD.
XX
XX
XX
XX

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PI Savitzky K, Khosravi R, Elazar M;
XX WPI; 2001-147341/15.
DR P-PSDB; AAB20173.
XX
PT Nucleic acid encoding alternative splicing variant of CD40 receptor,
PT useful for treating inflammatory diseases, autoimmune diseases, and graft
PT versus host reaction.
XX
XX Claim 1; Page 60; 70pp; English.
XX
XX The present sequence is that of mouse cDNA encoding splice variant
XX Mcd40Alt19 (see AAB20173) of the mouse CD40 receptor (CD40R). The variant
XX contains 165 N-terminal amino acids of the original CD40R sequence
XX including tumour necrosis factor receptor (TNFR) Cys repeats 1, 2 and 3,
XX and part of TNFR Cys repeat 4, with 30 alternative C-terminal amino
XX acids. It is missing part of TNFR repeat 4, the transmembrane domain and
XX the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of
XX human and murine CD40R, nucleic acids (see AAF30275-80) encoding them,
XX expression vectors, host cells and anti-CD40R antibodies are claimed.
XX Also claimed is a pharmaceutical composition consisting of an expression
XX vector comprising a CD40R nucleic acid, for treatment of diseases which
XX can be ameliorated, cured or prevented by either decreasing the level or
XX of at least 1 ligand of CD40R, by increasing the level of a CD40R variant.
XX variant, or by reducing the level of a CD40R variant. The diseases
XX include autoimmune diseases e.g. rheumatoid arthritis, systemic lupus
XX erythematosus, and multiple sclerosis, inflammatory diseases and graft
XX versus host disease. Also claimed are methods for detecting the presence
XX of a variant nucleic acid sequence of CD40R in a sample, for determining
XX the level of variant nucleic acid sequences of CD40R in a sample, and for
XX determining the ratio between the level of a CD40R variant nucleic acid
XX and the level of the original CD40R, e.g. using a nucleic acid chip
XX
XX Sequence 788 BP; 186 A; 221 C; 206 G; 175 T; 0 U; 0 Other;
SQ

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Query Match 67.6%; Score 547; DB 4; Length 788;
Best Local Similarity 95.3%; Fred. No. 6.7e-165;
Matches 584; Conservative 0; Mismatches 5; Indels 24; Gaps 1;

Qy      1 ATGGTGTCTTTTGGCTGTGGCTGTGGCGCTATGGGGCTGTTTGTACAGCGGTCCACTTA 60
Db      1 ATGGTGTCTTTTGGCTGTGGCTGTGGCGCTATGGGGCTGTTTGTACAGCGGTCCACTTA 60

Qy      61 GGGCAGTGTGTACGTGCAGTGACAAACAGTACTTCCAGATGCCAGTGTGTGATTG 120
Db      61 GGGCAGTGTGTACGTGCAGTGACAAACAGTACTTCCAGATGCCAGTGTGTGATTG 120

Qy      121 TGCCAGCCAGGAAGCCGACTGACAAAGCCACTGACAGCTCTTGAGAAAGACCAATGCCAC 180
Db      121 TGCCAGCCAGGAAGCCGACTGACAAAGCCACTGACAGCTCTTGAGAAAGACCAATGCCAC 180

Qy      181 CCATGTACTCAGGCGAATTCTCAGCCAGTGGAAACAGGGAGATTGCTGTCCACAGCAC 240
Db      181 CCATGTACTCAGGCGAATTCTCAGCCAGTGGAAACAGGGAGATTGCTGTCCACAGCAC 240

Qy      241 AGACACTGTGAACCCAGTGCCTGGGAGGGATCAAGGCTTCGGGTTAAG 300
Db      241 AGACACTGTGAACCCCA-----ATCAAGGCTTCGGGTTAAG 276

Qy      301 AAGGAGGACCGCAGAAATCAGACACTGTCTGTACTGTAAAGGAAGCAACAACCTCCACC 360
Db      277 AAGGAGGACCGCAGAAATCAGACACTGTCTGTACTGTAAAGGAAGCAACAACCTCCACC 336

Qy      361 AGCAGAGATTGCGAGGATGTCTCAGCACAGCCCTGTATCCCTGCTTGGAGTTATG 420
Db      337 AGCAGAGATTGCGAGGATGTCTCAGCACAGCCCTGTATCCCTGCTTGGAGTTATG 396

Qy      421 GAGATGCCACTGAGACCACTGATACCTGTGTATCCCTGCCAGTCGGCTTCTCTCC 480
Db      397 GAGATGCCACTGAGACCACTGATACCTGTGTATCCCTGCCAGTCGGCTTCTCTCC 456

Qy      481 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAAGCTTAAAGTCCCGGATGCG 540

```

Db 457 AATCAGTCATCACTTTTCGAAAGGTTTATCCTCGGACAAAGGTTTAAAGTCCCGGATCG 516  
 QY 541 AGCCCTGCTGGTCATCTCTGCGATCGGATCCTCATCCACTTTTCGGGGTGTTCCT 600  
 Db 517 AGCCCTGCTGGTCATCTCTGCGATCGGATCCTCATCCCGTTTTCGGGGTGTTCCT 576  
 QY 601 CTATATCAAAAAG 613  
 Db 577 CTATATCAGTGAG 589

## RESULT 5

AAAF30277  
 ID AAF30277 standard; cDNA; 934 BP.

XX AAF30277;

DT 30-APR-2001 (first entry)

XX Mouse CD40 receptor splice variant cDNA clone Mcd40-pPB1-1-5.

XX CD40 receptor; CD40R; mouse; splice variant; antiinflammatory;  
 KW immunosuppressive; antiarthritis; antirheumatic; dermatological;  
 KW neuroprotective; gene therapy; diagnosis; ss.

XX Mus musculus.

XX Key Location/Qualifiers  
 FH 33.503  
 FT /\*tag= a

XX WO200105967-A1.

PN 25-JAN-2001.

PD 19-JUL-2000; 2000WO-IL000427.

PF 20-JUL-1999; 99IL-00130989.

PR (COMP-) COMPUGEN LTD.

PA Savitzky K, Khosravi R, Elazar M;

PI WPI; 2001-147341/15.

XX P-PSDB; AAB20171.

PT Nucleic acid encoding alternative splicing variant of CD40 receptor,  
 useful for treating inflammatory diseases, autoimmune diseases, and graft  
 versus host reaction.

PS Claim 1; Page 59; 70pp; English.

XX The present sequence is that of mouse cDNA encoding splice variant Mcd40-  
 pPB1-1-5 (see AAB20171) of the mouse CD40 receptor (CD40R). The variant  
 contains 135 N-terminal amino acids of the original sequence including  
 CC tumour necrosis factor receptor (TNFR). Cys repeats 1 and 2, and part of  
 CC TNFR Cys repeat 3, with 21 alternative C-terminal amino acids. It is  
 CC missing the TNFR repeat 4, part of repeat 3, the transmembrane domain and  
 CC the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of  
 CC human and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
 CC expression vectors, host cells and antibodies are claimed. Also claimed  
 CC is a pharmaceutical composition consisting of an expression vector  
 CC comprising a CD40R nucleic acid, for treatment of diseases which can be  
 CC ameliorated, cured or prevented by either decreasing the level or of at  
 CC least 1 ligand of CD40R, by increasing the level of a CD40R variant, or  
 CC by reducing the level of a CD40R variant. The diseases include autoimmune  
 CC diseases e.g. rheumatoid arthritis, systemic lupus erythematosus, and  
 CC multiple sclerosis, inflammatory diseases and graft versus host disease.  
 CC Also claimed are methods for detecting the presence of a variant nucleic  
 CC acid sequence of CD40R in a sample, for determining the level of variant  
 CC nucleic acid sequences of CD40R in a sample, and for determining the  
 CC ratio between the level of a CD40R variant nucleic acid and the level of  
 CC the original CD40R, e.g. using a nucleic acid chip

XX SQ Sequence 934 BP; 246 A; 218 C; 231 G; 226 T; 0 U; 13 Other;  
 Query Match 53.1%; Score 429.2; DB 4; Length 934;  
 Best Local Similarity 84.5%; Pred. No. 5.Se-127;  
 Matches 541; Conservative 0; Mismatches 43; Indels 56; Gaps 3;  
 QY 1 ATGGTGCTTTTCTCGGCTGTGCGGCTATGGGCTATGGGCTGTGTTGACAGCGGTCCATCTA 60  
 Db 33 ATGGTGCTTTTCTCGGCTGTGCGGCTATGGGCTATGGGCTGTGTTGACAGCGGTCCATCTA 92  
 QY 61 GGGCAGTGTGTTACGTGCACTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
 Db 93 GGGCAGTGTGTTACGTGCACTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 152  
 QY 121 TGGCAGCCAGGAAGCCGACTGACAAAGCCACTGCACAGCTCTTGAGAGAGCCCAATGCCAC 180  
 Db 153 TGGCAGCCAGGAAGCCGACTGACAAAGCCACTGCACAGCTCTTGAGAGAGCCCAATGCCAC 212  
 QY 181 CCATGTGACTCAGGCGAATTTCTCAGCCCTGAGGAGAGATTGCTGTCCACAGCAC 240  
 Db 213 CCATGTGACTCAGGCGAATTTCTCAGCCCTGAGGAGAGATTGCTGTCCACAGCAC 272  
 QY 241 AGACACTGTGAACCCAGTGTGCTGGGCTGCTGGGAGAGGATCAAGGGCTTCGGGTTAAG 300  
 Db 273 AGACACTGTGAACCCA-----ATCAGGGCTTCGGGTTAAG 308  
 QY 301 AAGGAGGGCACCGCAGAAATCAGACACTGTCTGTACCTGTAAAGAGGACACAACTGCACC 360  
 Db 309 AAGGAGGGCACCGCAGAAATCAGACACTGTCTGTAAAGAGGACACAACTGCACC 368  
 QY 361 AGCAAGATTGCGAGGATGTGTCTCAGCACACGCCCTGTATCCCTGGCTTTGAGTTATG 420  
 Db 369 AGCAAGATTGCGAGGATGTGTCTCAGCACACGCCCTGTATCCCTGGCTTTGAGTTATG 428  
 QY 421 GAGATGCCACTGAGACCACTGATACCGTCTGTCTCCCTGCCAGTCGCTTCTTCTCC 480  
 Db 429 GAGATGCCCTGTGAGGATA-----GACTTGAGGTCCTAC 464  
 QY 481 AATCAGTCAATCACTTTTCGAAAAGTGTATCCCTGGACAAAGTTTAAAGTCCCGGATGG 540  
 Db 465 AGAAAGGAACGAGTCAGACTAATGTCTATCT-----GTGGTTTAAAGTCCCGGATGG 516  
 QY 541 AGCCCTGCTGGTCATCTCTGCTGATGGGATCCCTCATCACCATTTCGGGGTGTTCCT 600  
 Db 517 AGCCCTGCTGGTCATCTCTGCTGATGGGATCCCTCATCACCATTTCGGGGTGTTCCT 576  
 QY 601 CTATATCAAAAAGTGTGTCAGAAACCAAGGATAATGAG 640  
 Db 577 CTATATCAAAAAGTGTGTCAGAAACCAAGGATCTCGAG 616

## RESULT 6

ABQ74500  
 ID ABQ74500 standard; cDNA; 469 BP.

XX ABQ74500;

DT 21-OCT-2002 (first entry)

DE Mouse CD40 image clone nucleotide sequence SEQ ID NO:18.

XX Mouse; DNA array sequence selection; gene; cDNA microarray; probe;  
 KW immunology; tumour; cancer; cancer biology; immune cell; aging;  
 KW drug testing; infection; autoimmune disease; arthritis; allergy; vaccine;  
 KW ss.

XX Mus musculus.

XX WO200261135-A2.

XX 08-AUG-2002.

PD

XX

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PF 19-DEC-2001; 2001WO-US050618.
XX
XX
XX 19-DEC-2000; 2000US-00741238.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Lorenz M;
XX
XX WPI; 2002-608530/65.
XX
XX New composition comprising an array of cDNA probes immobilized on a solid
XX support, useful for diagnostic and screening procedures involving
XX immunologically-based sample materials, drug testing or monitoring
XX disease progression.
XX
XX Claim 1; Fig 3; 420pp; English.
XX
XX The present invention describes a composition comprising an array of cDNA
XX probes that are immobilised on a solid support, where the array comprises
XX at least 10-20 probes having sequences selected from the 29 sequences of
XX 192-4655 base pairs given in AB074483 to ABQ74511. Also described is a
XX method for selecting DNA sequences for a non-redundant microarray,
XX comprising: (a) providing sequence databases; (b) screening the databases
XX for DNA sequences specific for a species and a tissue found in the
XX species to generate a redundant sequence list; (c) removing redundant
XX sequences from the list to generate a non-redundant cluster list; (d)
XX categorising selected sequences from non-redundant cluster list into at
XX least one module list; and (e) selecting the best representative clones
XX based on the characteristics used to establish the parameters of the
XX module list. The composition comprising the microarrays is useful in
XX diagnostic and screening procedures involving immunologically-based
XX sample materials. It is used in experiments and screens in innate and
XX adaptive basic immunology, tumour immunology, cancer biology of immune
XX cells, aging, drug testing, infection immunology, autoimmune diseases,
XX arthritis, allergy, and vaccine development against these diseases. The
XX composition and method may be used in monitoring the progression of a
XX particular disease, in screening drug treatments for diseases, and in the
XX construction of non-redundant DNA microarrays for different species
XX
XX
XX Sequence 469 BP; 110 A; 120 C; 136 G; 103 T; 0 U; 0 Other;
XX
XX Query Match 39.7%; Score 312.8; DB 6; Length 469;
XX Best Local Similarity 99.4%; Pred. No. 1e-89;
XX Matches 314; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 494 TTTTCGAAAAGTGTATCCCTGACACAGGTTTAAAGTCCCGATGCGAGCCCTGCTGTC 553
XX 1 TTTTCGAAAAGTGTATCCCTGACACAGGTTTAAAGTCCCGATGCGAGCCCTGCTGTC 60
XX
XX 554 ATTCTCTGCTGTGATGGGCATCCTCATCCATTTTCGGGTGTTTCTATATCAAAAAG 613
XX 61 ATTCTCTGCTGTGATGGGCATCCTCATCCATTTTCGGGTGTTTCTATATCAAAAAG 120
XX
XX 614 GTGCTCAAGAACCAAGAGTAATGAGATGTTTACCCCTCGGCTGACGGCAGATCCC 673
XX 121 GTGCTCAAGAACCAAGAGTAATGAGATGTTTACCCCTCGGCTGACGGCAGATCCC 180
XX
XX 674 CAGGAGATGGAAGATTATCCCGGTCTATAACACCGCTGCTCCAGTGAGAGACATGTCAC 733
XX 181 CAGGAGATGGAAGATTATCCCGGTCTATAACACCGCTGCTCCAGTGAGAGACATGTCAC 240
XX
XX 734 GGGTGTGAGCTGTACACAGGAGGATGTTAAAGAGAGTGCGATCTCAGTGACGAGCGG 793
XX 241 GGGTGTGAGCTGTACACAGGAGGATGTTAAAGAGAGTGCGATCTCAGTGACGAGCGG 300
XX
XX 794 CAGGTGACACACAGCA 809
XX 301 CAGGTGACACACAGCA 316
XX
XX
XX RESULT 7
XX ADA25651
XX ID ADA25651 standard; DNA; 910 BP.
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XX ADA25651;
XX
XX 20-NOV-2003 (first entry)
XX
XX CD40 wild-type protein encoding DNA #SEQ ID 23.
XX
XX CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
XX inflammatory disease; cancer; atherosclerosis; acute injury; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 48..881
XX FT /*tag= a
XX FT /product= "CD40 wild-type protein"
XX
XX WO2003070768-A2.
XX
XX 28-AUG-2003.
XX
XX 24-FEB-2003; 2003WO-IB000665.
XX
XX 22-FEB-2002; 2002US-0358877P.
XX (COMP-) COMPUGEN LTD.
XX
XX Bernstein J, Mintz L, Eshel D;
XX WPI; 2003-697601/66.
XX P-PSDB; ADA25652.
XX
XX Protein, useful for preparing a composition for modulating CD40-CD154
XX interactions in an individual for treating chronic inflammatory disease,
XX cancer, atherosclerosis or acute injury.
XX
XX Disclosure; Page 90; 92pp; English.
XX
XX The invention relates to substantially pure CD40 splice variant proteins
XX which include tail sequences. Also disclosed is a pharmaceutical
XX composition comprising the protein and a carrier, an in vitro method of
XX detecting whether an individual is expressing the protein, and a method
XX for modulating CD40-CD154 interactions in an individual. The protein of
XX the invention is useful for preparing a composition for modulating CD40-
XX CD154 interactions in an individual for treating chronic inflammatory
XX disease, cancer, atherosclerosis or acute injury. The current sequence
XX represents CD40 wild-type protein encoding DNA.
XX
XX Sequence 910 BP; 212 A; 270 C; 240 G; 188 T; 0 U; 0 Other;
XX
XX Query Match 34.7%; Score 280.4; DB 8; Length 910;
XX Best Local Similarity 62.7%; Pred. No. 3.7e-79;
XX Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;
XX
XX 1 ATGGTGTCTTTGCTCGGCTGTGCGCTATGCGGCTGCTTGTGTGACAGCGGTCCATCTA 60
XX 48 ATGGTTCGTCTGCTCTGCACTGCGTCTCTGCGGCTGCTTGTGTGACCGCTGTCCATCCA 107
XX
XX 61 GGGCAGTGTGTTACGTGCGAGTGACAAACAGTACCTCCACGATGGCCAGTGTGTGATTG 120
XX 108 GAACCCACCTGATGCATGCAGAGAAAACAGTACCTAATAACAGTCACTGTCTTCTTTG 167
XX
XX 121 TGCCAGCCAGAAAGCCGACTGACAAAGCACTGCAAGTCTTTGAGAAAGCCAAATGCCAC 180
XX 168 TGCCAGCCAGCAAGAAACTGGTGAAGTCACTGCAAGAGTTCCTGAAACGGAAATGCCCTT 227
XX
XX 181 CCATGTGACTCAGGCGAATTCCTCAGCCAGTGGAAACAGGAGATTTCCTGTCCACAGCAC 240
XX 228 CTTTGGGTGAAGCGAATTCCTAGACACCTGGAAACAGAGACACACTGCCACAGCAC 287
XX
XX 241 AGACACTGTGAACCCAGTGTGCGTGGGCTGCTGGGAAGGGATCAAGGCTTCGGGTTAAG 300
XX 288 AAATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCAG 323
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Db 801 CAGGAGACTTTACATGGATGCAACCGTCACTCCAGGAGATGGCAAGAGAGTCGCATC 860  
 QY 779 TCAGTGCAGGAGCGGCAG 796  
 Db 861 TCAGTGCAGGAGAGACAG 878

RESULT 9  
 AAT14706  
 ID AAT14706 standard; cDNA; 1004 BP.  
 XX  
 AC AAT14706;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 30-OCT-1996 (first entry)  
 XX  
 DE Human CD40 antigen cDNA.  
 XX  
 KW Cell surface antigen; cloning; immunoselection; immunotherapy; therapy;  
 KW diagnosis; vector; CD40; COS; lymphocyte; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5506126-A.  
 XX  
 PD 09-APR-1996.  
 XX  
 PF 18-OCT-1993; 93US-00139273.  
 XX  
 PR 25-FEB-1988; 88US-00160416.  
 PR 13-JUL-1989; 89US-00379076.  
 PR 13-JUL-1990; 90US-00553759.  
 PR 01-DEC-1992; 92US-00938647.  
 XX  
 PA (GEMO) GEN HOSPITAL CORP.  
 XX  
 PI Seed B, Aruffo A;  
 XX  
 DR WPI; 1996-200279/20.  
 XX  
 PT Cloning of cDNA encoding cell surface antigen - useful for isolation of  
 PT diagnostic and therapeutic proteins.  
 XX  
 PS Example 8; Fig 16; 79pp; English.  
 XX  
 CC A cDNA clone (AAT14714) codes for human cell surface antigen CD40. It was  
 CC isolated using a rapid immunoselection method in which a cDNA library is  
 CC constructed in mammalian (e.g. COS) cells using novel expression vectors  
 CC (see also AAT14702 and AAT14705), and cells expressing the antigen are  
 CC selected using antibody-coated plates (panning). This immunoselection  
 CC cloning method, developed to clone genes for cell surface antigens of  
 CC human lymphocytes (see also AAT14703-04 and AAT14706-26), has general  
 CC appln. Cell surface antigens are obd. for diagnostic and therapeutic  
 CC use. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;

Query Match 34.7%; Score 280.4; DB 2; Length 1004;  
 Best Local Similarity 62.7%; Pred. No. 3.9e-79;  
 Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;

QY 1 ATGGTGTCTTTGCTCGGCTGTCGCGCTATGGGGTCTGTGTGTGACAGCGGTCCATCTA 60  
 Db 48 ATGGTTCGCTGCTGCTGCACTGGTCTCTCTGGGGTCTGTGTGTGACCGGTGCTCCATCCA 107  
 QY 61 GGGCAGTGTGTAGTGCAGTGACAAACAGTACTCCACGATGCGCCAGTCTGTGATTTG 120  
 Db 108 GAACACCCACTGTCATGACAGAAAACAGTACTTAATAACAGTCACTGCTCTTTT 167  
 QY 121 TGGCAGCCAGGAAGCCGACTGACAAAGCCACTGTCACAGCTCTTGAGAGACCCCAATGCCAC 180  
 Db 168 TGGCAGCCAGGACAGAAACTGGTGTGAGTGAAGTCTGACAGAGTTCACTGAAACGGAATGCCCT 227

QY 181 CCATGTGACTCAGGCGAATTTCTCAGCCAGTGGAAACAGGGAGATTCTGTCTCACCAGCAC 240  
 Db 228 CTTTGGGTGAAAGCGAATTTCTAGACACCTTGAACAGAGACACACTGCTCCACCAGCAC 287  
 QY 241 AGACACTGTGAACCCAGTGCCTGGGGTCTGCTGGAGAGGATCAAGGCTTCGGGTTAAG 300  
 Db 288 AAATACTCGCACCCCA-----ACCTAGGGCTTCGGGTTCCAG 323  
 QY 301 AAGGAGGCGCACCGCAGAAATCAGACACTGTCTGTACCTGTAAAGAGGACAACTGCACC 360  
 Db 324 CAGAGGCGCACCTCAGAAACAGACACCATCTGCACCTGTGAGAGAGGCTGSCACTGTACG 383  
 QY 361 AGCAAGGATTGGAGGCAATGTCTCAGCACACGCGCTGTATCCCTCGCTTTGGAGTTATG 420  
 Db 384 AGTGAAGGCTGTGAGAGCTGTCTCTGCACCGCTCATGCTCGCCCGCTTTGGGGTCAAG 443  
 QY 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTCTCATCCCTGCCAGTCGGCTTCTTCTCC 480  
 Db 444 CAGATTGCTCAGGGGTTTCTGTATACCATCTGCGAGCCCTGCCAGTCGGCTTCTTCTCC 503  
 QY 481 AATCAGTCACTCACTTTTCGAAAAGTGTATCCCTGGACAAGGTTTAA----- 527  
 Db 504 AATGTGTCACTGTCTTTCGAAAAATGTCACTCTGGACAGCTGTGAGACCAAGACCTG 563  
 QY 528 -----AGTCCCGGATG 538  
 Db 564 GTTGTGCAACAGGAGGCAAAACAGACTGATGTTGTCTGCTCCAGGATCGGCTG 623  
 QY 539 CGAGCCCTGCTGTCAATCTCTGTGTATGGGCACTCTCATCACCATTTCGGGGTGT 598  
 Db 624 AGAGCCCTGCTGTGATCCCATCATCTTTCGGGATCTGTTTGCATCTCTTGGTGTG 683  
 QY 599 CTCATATCAAAAAGTGTCTCAGAAACCAAGAGTAATGAGATGTTACCCCTGCGGCT 658  
 Db 684 GTCTTTTCAAAAAGTGTGCAAGAACCAACCAATTAAGGCCCCCCCCCAAGACGAG- 742  
 QY 659 CGACGGCAAGATCCCCAGGAGATGAAGATTATCCCGTTCATAACACCGTCTCCAGTG 718  
 Db 743 --ACCCAGGAGATCAATTTTCCGACGATCTTCTGCTCCAACTGCTGCTCCAGTG 800  
 QY 719 CAGGAGACACTGCGGGTGTCTCAGCCTGTCTACAGAGAGATGTTAAGAGAGTCCGATC 778  
 Db 801 CAGGAGACTTTACATGGATGCCAACCGGTCAACCAGGAGGATGGCAAGAGTCCGATC 860  
 QY 779 TCAGTGCAGGAGCGGCAG 796  
 Db 861 TCAGTGCAGGAGAGACAG 878

RESULT 10  
 AAV63454  
 ID AAV63454 standard; cDNA; 1004 BP.  
 XX  
 AC AAV63454;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-JUN-1999 (first entry)  
 XX  
 DE Human CD40 antigen cDNA.  
 XX  
 KW CD40; cell surface antigen; T cell antigen; T lymphocyte; human; cloning;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5830731-A.  
 XX  
 PD 03-NOV-1998.  
 XX  
 PF 21-MAY-1997; 97US-00861205.  
 XX  
 PR 25-FEB-1988; 88US-00160416.  
 PR 13-JUL-1989; 89US-00379076.

PR	23-MAR-1990;	90US-00498809.
PR	13-JUL-1990;	90US-00553759.
PR	01-DEC-1992;	92US-00983647.
XX	(GEO ) GEN HOSPITAL CORP.	
PA		
PI	Seed B,	Arufo A;
XX		
DR	WPI; 1998-609251/51.	
XX		
PT	New cloning vector and poly:linker - based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially human lymphocyte antigenic sequences.	
PT		
PS	Example 8; Fig 16; 75pp; English.	
XX		
CC	This nucleotide sequence comprises human CD40 antigen cDNA. It was isolated by a novel method for cloning cDNAs from mammalian expression libraries that is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate, such as a culture dish. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell. It has been used to clone genes (see AAU63442-63) encoding cell surface antigens from mammalian lymphocytes (see AAU80440-55). The isolated genes can be expressed in a prokaryotic or eukaryotic host cells to produce the encoded protein. The invention also provides high efficiency expression vectors (see AAU63441 and AAU63444), which allow the generation of very large mammalian expression libraries. The purified genes and proteins are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, diseases, and disorders of animals, including humans. (Updated on 25-MAR-2003 to correct PR field.)	
XX		
SQ	Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;	
	Query Watch	34.7%; Score 280.4; DB 2; Length 1004;
	Best Local Similarity	62.7%; Pred. No. 3.9e-79;
	Matches 538; Conservative	0; Mismatches 231; Indels 89; Gaps 3
QY	1	ATGGTGCTTTGCCCTCGGCTGCGCGTATGGGGCTGTGGTGTGCACGGGTCCATCTA 50
Db	48	ATGTTTCGTCTGCCCTTCAGTGTGCTCTGGGGCTGCTGTGACCGTGTCCATCCA 107
QY	61	GGCGAGTGTGTTACGTGCAGTGCAAAACAGTAACCTCCAGTGGCAGTGTGTGATTGG 120
Db	108	GAACCACCCACTGCATGCAGAGAAAAACAGTACCTATAAACAGTCAGTGCTGTTCTTGG 167
QY	121	TGCCAGCCAGGAGCGGACTCACAGCCACTGCACAGCTCTTGAGAAGACCCCATGCCAC 180
Db	168	TGCCAGCCAGGACAGAAACTGGTAGTGACTGCACAGAGTTCACTGAAAACGGGAATGCCCT 227
QY	181	CCATGTGACTCAGGCGGAATTTCTAGCCCCAGTGGAAACAGGAGAGATTGCCTGTCCACAGCAC 240
Db	228	CCTTGGGTTGAAGCGAATTCCTAGACACCTGGAAACAGAGAGACACACTGCCACAGCAC 287
QY	241	AGACACTGTGAACCCAGTGCCTGGGGCTGCTCGTGGAAAGGGATCAAGGGCTTGGGGTTAAG 300
Db	288	AAATACTCGGACCCCA-----ACCTAGGGCTTCGGGTCAG 323
QY	301	AAGGAGGGGACCGCAGAAATCAGACACTGTCTGTACCTGTGAAGAAAGCAACAACATGCACC 360
Db	324	CAGAAGGCACCTCAGAAACAGACACCAATCTGACCTTGTGAAGAGCTGGCACTGTACG 383
QY	361	AGCAAGGATTCGAGGCGATGTCCTCAGCACACGCCCTGTATCCTCGCTTTGGAGTTATG 420
Db	384	AGTAGGGCTGTGAGAGCTGTGTCTGCACCGCTCATGCTCGCCCGGCTTTGGGGTCAAG 443
QY	421	GAGATGGCCACTGAGACCACTGATACCGTCTGTATCCCTGCCAGTCGGCTTCTCTCC 480
Db	444	CAGATTGCTACAGGGGTTTCTTGATACCATCTGCGAGCCCTGCCAGTCGGCTTCTCTCCC 503
QY	481	AATCAGTCAATCACTTTTCGAAAGTGTATCCCTGGCAAGGTTTAA----- 527



QY 1 ATGTGTCCTTTGCTGGCTGTGCGGCTATATGGGCTGCTTTGTCAGACGGTCCATCTA 60  
 DB |||||  
 QY 48 ATGGTTCGCTGCTCTGTCAGTGGCTCTCTGGGCTGCTTCTGTCAGCGTGCATCCA 107  
 DB |||||  
 QY 61 GGGCAGTGTGTACGTGTCAGTGCACAAAGTACTCCACGATGGCCAGTGTGATTTG 120  
 DB |||||  
 QY 108 GAACACCCACTGCAATGTCAGAGAAACAGTACCTTAATAACAGTCAGTGTGTTCTTTG 167  
 DB |||||  
 QY 121 TGCCAGCCAGGAAGCCGCTGCAAGCCACTGCACAGCTCTTGAGAAGACCCCAATGCCAC 180  
 DB |||||  
 QY 168 TGCCAGCCAGGACAGAACTGTGTAGTGTACTGCACAGAGTTCACCTGAAACGGAATGCCCTT 227  
 DB |||||  
 QY 181 CCATGTGACTCAGGCGAATTTCTAGCCAGTGTGAACAGGAGATTCGCTGTCCACGAC 240  
 DB |||||  
 QY 228 CCTTGGCGTGAAGCGAATTTCTAGACACCTGGAACAGAGACACACTGCCACACGAC 287  
 DB |||||  
 QY 241 AGACACTGTGAACCCAGTGGCTGCTGGGCTGCTTGGGAAGGATCAAGGGCTTCGGGTAAAG 300  
 DB |||||  
 QY 288 AATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323  
 DB |||||  
 QY 301 AAGAGGGCAGCCGAGAAATCAGACACTGTGTACTGTGTAAGAGGACAACTGCACC 360  
 DB |||||  
 QY 324 CAGAGGGCACCTTCAGAAACAGACACCACTGTGACCTGTGAAGAGGCTGGCACTGTAG 383  
 DB |||||  
 QY 361 AGCAAGGATTTGGAGCATGTCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG 420  
 DB |||||  
 QY 384 AGTGGCTGTGAGAGCTGTCTGACCCGCTCATGCTCGCCGCTTTGGGTCAG 443  
 DB |||||  
 QY 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTCTATCCCTGCCAGTGGCTTCTTCC 480  
 DB |||||  
 QY 444 CAGATTGCTACAGGGGTTTCTGATACCACTGTGAGCCCTGCCAGTGGCTTCTTCC 503  
 DB |||||  
 QY 481 AATCAGTCATCTTTTTCGAAAGTGTATCCCTGGACAAAGTTTAA----- 527  
 DB |||||  
 QY 504 AATGTCTATCTGCTTTTCGAAAGTGTATCCCTGGACAAAGTGTGAGACCAAGACCTG 563  
 DB |||||  
 QY 528 -----AGTCCCGGATG 538  
 DB |||||  
 QY 564 GTTGTGCACAGGACGACCAACAGACTGATGTTGCTGTGGTCCCGAGATCGGCTG 623  
 DB |||||  
 QY 539 CGAGCCCTGCTGTCATCTCTGTGATGGGATCTCTCATCACCATTGTTGGGCTGTTT 598  
 DB |||||  
 QY 624 AGAGCCCTGCTGTGATCCCATCATCTTTCGGGATCTCTTGGCATCTCTTGGTGTG 683  
 DB |||||  
 QY 599 CTCATATCAAAAAGTGTGCAAGAACCAAGGATAATGAGATGTACCCCTCGGCT 658  
 DB |||||  
 QY 684 GTCTTATCAAAAAGTGTGCAAGAACCAAGGATAATGAGATGTACCCCTCGGCT 742  
 DB |||||  
 QY 659 CGACGGCAAGATCCCGAGGATGGAAGATTATCCCGGTCAATAACACCGCTCTCCAGTG 718  
 DB |||||  
 QY 743 --ACCCAGGAGATCAATTTTCCGACGATCTTCTGGCTCCACACTGCTCTCCAGTG 800  
 DB |||||  
 QY 719 CAGGACACTGCACGGGTGTGACCTGTCTACACAGGAGATGTAAGAGATGTCATC 778  
 DB |||||  
 QY 801 CAGGAGACTTTACATGATGCAACCGGTGACCCAGGAGATGGCAAGAGATGCGCATC 860  
 DB |||||  
 QY 779 TCAGTGCAGGAGCGGACG 796  
 DB |||||  
 QY 861 TCAGTGCAGGAGACAG 878  
 DB |||||

RESULT 13  
 AA223432  
 ID AA223432 standard; DNA; 1004 BP.  
 XX AC AA223432;  
 XX AC  
 DT 19-JAN-2000 (first entry)  
 DE Human CD40 DNA.  
 XX KW Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;  
 KW huntingtin polypeptide; Machado-Joseph disease; SCAL; SCA2; SCA6;

KW atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;  
 KW Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;  
 KW dentatorubropallidoluysian atrophy; cell proliferation; cell survival;  
 KW neoplastic; malignant; autoimmune; fibrotic; CD40; ss.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 48..881  
 FT /\*tag= a  
 FT /product= "CD40"  
 XX  
 PW WO9945944-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 11-MAR-1999; 99WO-US005250.  
 XX  
 PR 12-MAR-1998; 98US-00041886.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Bredesen DE, Rabizadeh S;  
 XX  
 DR WPI; 1999-561617/47.  
 DR P-PSDB; AAY33499.  
 XX  
 PT New proapoptotic dependence peptides, used to develop products for  
 PT treating, e.g. Alzheimer's disease.  
 XX  
 PS Disclosure; Page 168-169; 199pp; English.  
 XX  
 CC This invention describes novel pure proapoptotic dependence peptides  
 CC which comprise a sequence of an active dependence domain selected from  
 CC dependence polypeptides consisting of p75NTR, androgen receptor, DCC,  
 CC huntingtin polypeptide, Machado-Joseph disease gene product, SCAL, SCA2,  
 CC SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable of  
 CC inducing cell death and can be used to develop products to mediate or  
 CC inhibit apoptosis. The methods can be used for reducing the severity of a  
 CC proapoptotic dependence domain mediated pathological conditions e.g.  
 CC Huntington's disease, Alzheimer's disease, Kennedy's disease,  
 CC spinocerebellar ataxia, dentatorubropallidoluysian atrophy, Machado-  
 CC Joseph disease, stroke or head trauma. They can also be used for reducing  
 CC the severity of a pathological condition mediated by upregulated cell  
 CC proliferation or cell survival e.g. neoplastic, malignant, autoimmune or  
 CC fibrotic conditions. This sequence encodes the human CD40 polypeptide  
 CC described in the method of the invention  
 XX  
 SQ Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;  
 Query Match 34.7%; Score 280.4; DB 2; Length 1004;  
 Best Local Similarity 62.7%; Pred. No. 3.9e-79;  
 Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;  
 QY 1 ATGTGTCCTTTGCTGGCTGTGCGGCTATATGGGCTGCTTTGTCAGACGGTCCATCTA 60  
 DB |||||  
 QY 48 ATGGTTCGCTGCTCTGTCAGTGGCTCTCTGGGCTGCTTCTGTCAGCGTGCATCCA 107  
 DB |||||  
 QY 61 GGGCAGTGTGTACGTGTCAGTGCACAAAGTACTCCACGATGGCCAGTGTGATTTG 120  
 DB |||||  
 QY 108 GAACACCCACTGTATGCAGAGAAACAGTACCTTAATAACAGTCAGTGTGTTCTTTG 167  
 DB |||||  
 QY 121 TGCCAGCCAGGAAGCCGCTGCAAGCCACTGCACAGCTCTTGAGAAGACCCCAATGCCAC 180  
 DB |||||  
 QY 168 TGCCAGCCAGGACAGAACTGGTGTAGTGTACTGCACAGAGTTCACCTGAAACGGAATGCCCTT 227  
 DB |||||  
 QY 181 CCATGTGACTCAGGCGAATTTCTAGCCAGTGTGAACAGGAGATTCGCTGTCCACGAC 240  
 DB |||||  
 QY 228 CCTTGGCGTGAAGCGAATTTCTAGACACCTGGAACAGAGACACACTGCCACACGAC 287  
 DB |||||  
 QY 241 AGACACTGTGAACCCAGTGGCTGCTGGGCTGCTTGGGAAGGATCAAGGGCTTCGGGTAAAG 300  
 DB |||||  
 QY 288 AATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323  
 DB |||||

QY 301 AAGAGGGCCCGCAGAAATCAGACACTGTCTGTACCTGTGTAAGGAGGACAACTGCACC 360  
 Db 324 CAGAAGGGCCACCTCAGAAACAGACACCATCTGCACCTGTGAAGAGGCTGGCACTGTACG 383  
 QY 361 AGCAAGGATCCGAGGATGTGCTCAGACACGCGCTGTATCCCTGGCTTTGAGATTATG 420  
 Db 384 AGTGAAGGCTGTGAGAGCTGTCTCGACCGCTCATGCTCGCCGCTTTGGGGTCAAG 443  
 QY 421 GAGATGGCCATGAGACCATGATACCGTGTGTATCCCTGCCCGAGTCGCTTCTCTCC 480  
 Db 444 CAGATTGCTACAGGGGTTCTGTATACCATCTCGAGCGCTGCCAGTCGGCTTCTCTCC 503  
 QY 481 AATCAGTCATCATCTTTTGGAAAGTGTATCCCTGGACAGGTTTAA-----527  
 Db 504 AATGTGTATCTGCTTTTGGAAAGTGTATCCCTTTGGACAGCTGTGAGACCAAGACCTG 563  
 QY 528 -----AGTCCCGGATG 538  
 Db 564 GTTGTGCAACAGGAGGACACAAACAGACTGATGTTGTCTGTGTCCTCCAGGATCGGCTG 623  
 QY 539 CGAGCCCTGCTGTCATCTCTGTCGTGATGGGATCCTCATCACCATTTCGGGGTGT 598  
 Db 624 AGAGCCCTGGTGGTATCCCATCATCTTCGGGATCCTGTTGCCATCTCTTTGGTGTG 683  
 QY 599 CTCTATATCAAAAAGGTGGTCAAGAAACCAAGAAAGTAAATGAGATGTTACCCCTCGCGGCT 658  
 Db 684 GTCTTTATCAAAAGGTGGCCAGAGCAACCAATGAAGCCCCCACCACCCAGCAGGA- 742  
 QY 659 CGAGCGCAAGATCCCGAGGAGATGGAAGATATCCCGGTCTATACACCGCTGTCCAGTG 718  
 Db 743 --ACCCCGAGGAGATCAATTTTCCCGAGGATCTTCTCGGCTCCACACTGTGCTCCAGTG 800  
 QY 719 CAGGAGACACTGCACGGGTGTCAGCCTGTGCACAGGAGGATGTTAAAGAGAGTCGCATC 778  
 Db 801 CAGAGACTTTACATGATGCCAACCGGTACCCAGGAGGATGGCAAGAGAGTCCGATC 860  
 QY 779 TCAGTCAGGAGCGGCAG 796  
 Db 861 TCAGTCAGGAGAGACAG 878

RESULT 14  
 AAA50590  
 ID AAA50590 standard; cDNA; 1004 BP.  
 XX AC AAA50590;  
 XX DT 19-DEC-2000 (first entry)  
 XX DE Human cell surface antigen CD40 cDNA.  
 XX KW CD40; cell surface antigen; human; immunoselection; panning;  
 KW immunodiagnosis; diagnosis; immunotherapy; gene therapy; immune disorder;  
 KW infection; asthma; immune-complex disease; amyloidosis;  
 KW multiple sclerosis; parasitic disease; ss.  
 XX OS Homo sapiens.  
 XX PN US6111093-A.  
 XX PD 29-AUG-2000.  
 XX PF 28-OCT-1998; 98US-00181612.  
 XX PR 25-FEB-1988; 88US-00160416.  
 PR 13-JUL-1989; 89US-00379076.  
 PR 23-MAR-1990; 90US-00498809.  
 PR 13-JUL-1990; 90US-00553759.  
 PR 01-DEC-1992; 92US-00983647.  
 XX PA (GEHO ) GEN HOSPITAL CORP.  
 XX

PI Stamenkovic I, Seed B;  
 XX WPI; 2000-586382/55.  
 XX  
 PT Isolated nucleic acid molecule encoding the CD19 cell surface antigen,  
 PT useful for immunodiagnosis and immunotherapy of immune-mediated  
 PT infections or disorders, e.g. asthma, immune-complex disease, parasitic  
 PT diseases.  
 XX  
 PS Claim 1; Fig 16; 75pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding human cell surface antigen  
 CC (CSA) CD40. The cDNA was isolated using a rapid immunoselection cloning  
 CC method of the invention, designed to isolate CSA cDNAs. The method is  
 CC based upon transient expression of a CSA in eukaryotic cells and physical  
 CC selection of cells expressing the antigen by adhesion to (panning on) an  
 CC antibody-coated substrate such as a culture dish. CSA nucleic acids  
 CC isolated by the method of the invention, and the proteins they encode,  
 CC are useful for immunodiagnostic and immunotherapeutic applications,  
 CC including the diagnosis and treatment of immune-mediated infections,  
 CC diseases, and disorders in animals, including humans. These disorders  
 CC include asthma, immune-complex disease, amyloidosis, parasitic diseases  
 CC or multiple sclerosis  
 XX  
 SQ Sequence 1004 BP; 230 A; 287 C; 276 G; 201 T; 0 U; 0 Other;  
 Query Match 34.7%; Score 280.4; DB 3; Length 1004;  
 Best Local Similarity 62.7%; Pred. No. 3.9e-79;  
 Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;  
 QY 1 ATGGTGTCTTTTGGCTGTGCGCTATGGGGCTGCTTGTGACAGCGGTCCATCTA 60  
 Db 48 ATGGTTCGTCTGCTCTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107  
 QY 61 GGGCAGTGTGTACGTGAGTGACAAACAGTACCTCCACGATGCCAGTGTGTTG 120  
 Db 108 GAACACCCACTGATGACGAGAAACAGTACTATAACACTGCTGTCTTCTTTG 167  
 QY 121 TGCCAGCCAGGAAGCCGACTGACAGCCACTGACAGCTCTTTGAGAAAGACCAATGCAC 180  
 Db 168 TGCCAGCCAGGACAGAAACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 227  
 QY 181 CCATGTGACTCAGCGGATTTCTAGCCCGAGTGGAACAGGAGATTCGCTGTCACGAC 240  
 Db 228 CTTTGGGTGAAAGCGAATCTTAGACACCTGGAAACAGAGACACACTGCCACGAC 287  
 QY 241 AGACACTGTGAACCCAGTGCCTGGGGCTGCTGGGAGGATCAAGGGCTTCGGGTTAAG 300  
 Db 288 AAATACTCGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323  
 QY 301 AAGAGGGCCCGCAGAAATCAGACACTGTCTGTACCTGTGTAAGGAGGACAACTGCACC 360  
 Db 324 CAGAAGGGCCACCTCAGAAACAGACACCATCTGCACCTGTGAAGAGGCTGGCACTGTACG 383  
 QY 361 AGCAAGGATTCGAGGATGTGCTCAGACACGCGCTGTATCCCTGGCTTTGAGATTATG 420  
 Db 384 AGTGAAGGCTGTGAGAGCTGTCTCGACCGCTCATGCTCGCCGCTTTGGGGTCAAG 443  
 QY 421 GAGATGGCCATGAGACCATGATACCGTGTGTATCCCTGCCCGAGTCGCTTCTCTCC 480  
 Db 444 CAGATTGCTACAGGGGTTTCTGATACCATCTCGAGCGCTGCCAGTCGGGCTTCTCTCC 503  
 QY 481 AATCAGTCATCATCTTTTGGAAAGTGTATCCCTTTGGACAGGTTTAA-----527  
 Db 504 AATGTGTATCTGCTTTTGGAAAGTGTATCCCTTTGGACAGCTGTGAGACCAAGACCTG 563  
 QY 528 -----AGTCCCGGATG 538  
 Db 564 GTTGTGCAACAGGAGGACACAAACAGACTGATGTTGTCTGTGTCCTCCAGGATCGGCTG 623  
 QY 539 CGAGCCCTGCTGTCATCTCTGTCGTGATGGGATCCTCATCACCATTTCGGGGTGT 598  
 Db 624 AGAGCCCTGGTGGTATCCCATCATCTTCGGGATCCTGTTGCCATCTCTTTGGTGTG 683

QY 599 CTCATATCAAAAGGTGCTCAAGAAACCAAGGATAATGAGATGTACCCCTCGGCT 658  
 DB 684 GTCCTTATCAAAAGGTGCTCAAGAAACCAAGGATAATGAGATGTACCCCTCGGCT 742  
 QY 659 CGAGCGCAAGATCCCGAGAGATGGAAGATTATCCGGTCAATAACCGCTGCTCCAGTG 718  
 DB 743 --ACCCAGGAGATCAATTTTCCGACGATCTTCCGCTCCCAACACTGCTCCAGTG 800  
 QY 719 CAGGAGACACTGCACGGGTGCTCAGCTGTACACAGGAGGATGTTAAAGAGATGCGATC 778  
 DB 801 CAGGAGACTTTACATGATGATGCAACCGTCAACGAGGAGATGGAAGAGATGCGATC 860  
 QY 779 TCAGTGCAGGAGCGGAG 796  
 DB 861 TCAGTGCAGGAGACAG 878  
 RESULT 15  
 AA247769  
 ID AA247769 standard; DNA; 1004 BP.  
 XX  
 AC AA247769;  
 XX  
 DT 02-MAR-2000 (first entry)  
 XX  
 DE Human CD40 nucleotide sequence SEQ ID NO:85.  
 KW Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;  
 KW expression; immune disease; inflammatory disease; immunomodulatory;  
 KW anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;  
 KW anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;  
 KW hyperproliferative disease; autoimmune disease; rheumatoid arthritis;  
 KW inflammatory bowel disease; asthma; psoriasis; cancer; tumour; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9957320-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 22-APR-1999; 99WO-US008765.  
 XX  
 PR 01-MAY-1998; 98US-00071433.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Cowser LM;  
 XX  
 DR WPI; 2000-062158/05.  
 XX  
 PT Antisense molecules directed against nucleic acid encoding human CD40,  
 for treating e.g. immune, inflammatory or hyperproliferative diseases.  
 XX  
 PS Example 9; Page 97-98; 102pp; English.  
 XX  
 CC AA247685 to AA247768 represent phosphorothioate antisense  
 CC oligonucleotides targeted to human CD40, which can be used to inhibit the  
 CC expression of human CD40. CD40 is involved in lymphocyte activation,  
 CC tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or  
 CC prevent immune-associated diseases (specifically guest vs. host disease,  
 CC allograft rejection or autoimmune diseases); inflammation (specifically  
 CC asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel  
 CC disease or psoriasis) or hyperproliferation (specifically cancer and  
 CC tumours). the antisense oligonucleotides are also useful as diagnostic  
 CC and research reagents. AA247769 represents the human CD40 nucleotide  
 CC sequence. AA247770 to AA247772 represent human CD40 forward and reverse  
 CC PCR primers, and a human CD40 PCR probe, respectively. AA247773 to  
 CC AA247775 represent other PCR primers and a probe used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;

Query Match 34.7%; Score 280.4; DB 3; Length 1004;  
 Best Local Similarity 62.7%; Pred. No. 3.9e-79;  
 Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;

QY 1 ATGTTGTTCTTGGCTCGGCTGTGGCGCTATGGGCTGCTTGTGACAGCGGTCCATCTA 60  
 DB 48 ATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107  
 QY 61 GGGCAGTGTGTAGTGCAGTGCACAAACAGTACCTCCACGATGGCCAGTGTGTGATTG 120  
 DB 108 GAACACCCACTGATGCAGAGAAACAGTACCTAATAACAGTCACTGTCTGTCTTTG 167  
 QY 121 TGCAGCCAGGAAGCCGACTGACAAAGCCACTGCACAGCTCTTGAGAAAGACCCCAATGCCAC 180  
 DB 168 TGCAGCCAGGACAGAAACCTGGTGAAGTCACTGACAGAGTTCACTGAACCGGAATGCTT 227  
 QY 181 CCATGTGACTCAGGCGAATTTCTACGCCAGTGGAAACAGGAGATTCGCTGTACACGAC 240  
 DB 228 CTTGCGGTGAAGCAATTTCTAGACACCTGGAACAGAGACACTGCCACAGAC 287  
 QY 241 AGACACTGTGAACCCAGTGTGGGCTGCTGGGAAGGATCAAGGGCTTCGGGTTAAG 300  
 DB 288 AATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCAG 323  
 QY 301 AAGAGGGCCACGAGAAATCAGACACTGTCTGTACCTGTAAAGAGACACACTGCACC 360  
 DB 324 CAGAAGGGCACTCAGAAACAGACACCATCTGCACCTGTGAAGAGGCTGGCACTGTACG 383  
 QY 361 AGCAAGGATTGCGAGGCAATGTCTCAGCACACGCGCTGTATCCCTGGCTTTGGAGTTATG 420  
 DB 384 AGTGAGCCCTGTGAGAGTGTCTCTCAGCGCTCATGCTCGCCGCTTTGGGTTCAAG 443  
 QY 421 GAGATGGCACTGAGACACTGATACCGTGTGTATCCCTGCCAGCTCGGCTTTCTTCC 480  
 DB 444 CAGATTGCTACAGGGGTTTCTGATACCATCTCGAGGCTTGCACAGTGTGGCTTCTTCTCC 503  
 QY 481 AATCAGTCACTCACTTTTCGAAAGTGTATCCCTGGCAAGGTTTAA----- 527  
 DB 504 AATGTGATCTGCTTTTCGAAAGTGTATCCCTTTGGACAGCTGTGAGACCAAGACCTG 563  
 QY 528 -----AGTCCCGGATG 538  
 DB 564 GTTGTCAACAGGCGGCAACAAACAGACTGATGTTGTGTGTCCTCCAGGATCGGCTG 623  
 QY 539 CGAGCCCTGTGCTCATCTCTGTGATGGGATCTCATCACCATTTCGGGTTGTTT 598  
 DB 624 AGACCCCTGGTGTATCCCATCATCTTGGGATCTGTTTGGCATCTCTTTGGTGTG 683  
 QY 599 CTCTATATCAAAAGGTGCTCAAGAAACCAAGGATAATGAGATGTTACCCCTCGGCT 658  
 DB 684 GTCCTTATCAAAAGGTGGCCAGAGCAACCAATAAGGCCCCCAAGCAGGA- 742  
 QY 659 CGAGGCAAGATCCCGAGGAGATGGAAGATTATCCGGTCAATAACAGGCTGCTCCAGTG 718  
 DB 743 --ACCCAGGAGATCAATTTTCCCGAGATCTTCTGCTCCAAACACTGCTGCTCCAGTG 800  
 QY 719 CAGGAGACTGCACGGGTGTCAGCTGTACACAGGAGGATGTTAAAGAGATGCGATC 778  
 DB 801 CAGGAGACTTTACATGATGATGCAACCGTCAACGAGGAGATGGAAGAGATGCGATC 860  
 QY 779 TCAGTGCAGGAGCGGAG 796  
 DB 861 TCAGTGCAGGAGACAG 878

Search completed: July 25, 2004, 01:05:53  
 Job time : 404 secs



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OM nucleic - nucleic search, using sw model

Run on: July 24, 2004, 23:50:12 ; Search time 2499 Seconds

(without alignments)

9667.269 Million cell updates/sec

Title: US-10-031-607-6

Perfect score: 809

Sequence: 1 atgtgtctttgcctcggtc.....gcggcaggtgacagacagca 809

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_estl.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rcd.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gssl.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	679	83.9	2901	11	AK089861	AK089861 Mus muscu
2	670	82.8	947	13	BU516152	BU516152 AGENCOURT
3	494.8	61.2	692	13	BY751423	BY751423 BY751423
4	467	57.7	663	13	BY743050	BY743050 BY743050

5	464.6	57.4	647	13	BY745486	BY745486
6	464.6	57.4	665	13	BY751441	BY751441
7	463.6	57.3	649	13	BY744299	BY744299
8	448.4	55.4	655	13	BY745292	BY745292
9	444.6	55.0	941	10	BF166137	BF166137
10	443.6	54.8	656	13	BY745260	BY745260
11	380.6	47.0	603	14	CB547441	CB547441
12	377.4	46.8	440	13	BY211683	BY211683
13	370.4	45.8	435	13	BY041398	BY041398
14	355.4	43.9	429	13	BY211594	BY211594
15	352.8	43.6	460	13	BY259264	BY259264
16	344.2	42.5	409	13	BY211153	BY211153
17	343.8	42.5	433	13	BY211500	BY211500
18	343	42.4	390	13	BY212394	BY212394
19	339.4	42.0	402	13	BY217640	BY217640
20	339	41.9	421	13	BY217850	BY217850
21	337	41.7	430	13	BY211470	BY211470
22	337	41.7	576	10	BF566819	BF566819
23	335.4	41.5	401	13	BY161491	BY161491
24	334.2	41.3	418	13	BY217907	BY217907
25	332	41.0	396	13	BY164847	BY164847
26	330	40.8	392	13	BY212378	BY212378
27	328.2	40.6	399	13	BY218151	BY218151
28	325	40.2	400	13	BY158588	BY158588
29	320.8	39.7	416	13	BY165294	BY165294
30	320.4	39.6	397	13	BY058815	BY058815
31	319.6	39.5	545	12	BG276290	BG276290
32	318.4	39.4	385	13	BY165017	BY165017
33	316	39.1	376	13	BY160241	BY160241
34	312.8	38.7	469	9	AI385482	AI385482
35	312.4	38.6	377	13	BY042027	BY042027
36	310.4	38.4	378	13	BY165819	BY165819
37	310	38.3	375	13	BY213466	BY213466
38	307.4	38.0	372	13	BY038457	BY038457
39	307.4	38.0	372	13	BY222909	BY222909
40	307	37.9	370	13	BY161002	BY161002
41	307	37.9	370	13	BY168925	BY168925
42	307	37.9	381	13	BY216263	BY216263
43	305.4	37.8	367	13	BY216777	BY216777
44	305	37.7	352	13	BY223332	BY223332
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#### ALIGNMENTS

RESULT 1	AK089861	2901 bp	mRNA	linear	HTC 20-SEP-2003
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DEFINITION	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone.F830034E13 product:Tumor necrosis factor receptor superfamily member 5, full insert sequence.				
ACCESSION	AK089861	GI:26354702			
VERSION	AK089861.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Math. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				

```

3
REFERENCE
AUTHORS
  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
  Konno,H., Akiyama,O., Nishi,K., Kitesunai,T., Tashiro,H., Itoh,M.,
  Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
  Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
  Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
  Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
  Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE
  RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL
MEDLINE
  Genome Res. 10 (11), 1757-1771 (2000)
PUBMED
  11076861
REFERENCE
AUTHORS
4
  The RIKEN Genome Exploration Research Group Phase II Team and the
  PANTOM Consortium.
TITLE
  Functional annotation of a full-length mouse cDNA collection
JOURNAL
MEDLINE
  Nature 409, 685-690 (2001)
PUBMED
  11076861
REFERENCE
AUTHORS
5
  The PANTOM Consortium and the RIKEN Genome Exploration Research
  Group Phase I & II Team.
TITLE
  Analysis of the mouse transcriptome based on functional annotation
  of 60,770 full-length cDNAs
JOURNAL
MEDLINE
  Nature 420, 563-573 (2002)
PUBMED
  12000000
REFERENCE
AUTHORS
  Adachi,J., Aizawa,K., Akimura,T., Arawaka,T., Bono,H., Carninci,P.,
  Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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  Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
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  Muramatsu,M. and Hayashizaki,Y.
TITLE
  Direct Submission
JOURNAL
MEDLINE
  Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
  Physical and Chemical Research (RIKEN), Laboratory for Genome
  Exploration-Research Group, RIKEN Genomic Sciences Center (GSC),
  RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
  Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
  URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
  Fax:81-45-503-9216)
COMMENT
  cDNA library was prepared and sequenced in Mouse Genome
  Encyclopedia Project of Genome Exploration Research Group in Riken
  Genomic Sciences Center and Genome Science Laboratory in RIKEN.
  Division of Experimental Animal Research in Riken contributed to
  prepare mouse tissues.
  Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
  Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
  Trust/MRC building Addenbrookes Hospital Cambridge) whose
  assistance we gratefully acknowledge.
  Please visit our web site for further details.
  URL:http://genome.gsc.riken.go.jp/
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RESULT 2
LOCUS BU516152 947 bp mRNA linear EST 12-SEP-2002
DEFINITION AGENCOURT_10120358 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6512860 5', mRNA sequence.
ACCESSION BU516152
VERSION BU516152.1 GI:22823678
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 947)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14085 row: k column: 05
High quality sequence stop: 723.
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size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 82.8%; Score 670; DB 13; Length 947;
Best Local Similarity 89.4%; Pred. No. 3.6e-194;
Matches 779; Conservative 0; Mismatches 6; Indels 86; Gaps 2;
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DB 5 ATGGTGCTCTTTCCTCGGCTGTGCGCGCTATGCGGCTGCTTTGACAGCGGTCCATCTA 64
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DB 245 AGACACTGTGACCCCA-----ATCAGGGGCTTCGGGTAAAG 280
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QY 361 AGCAAGGATGGAGGCAATGTGCTCAGACACAGCCCTGTATCCCTGGCTTTGGAGTTATG 420

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DB 401 GAGATGCCACTCAGACCACTGATACCGTCTGTCATCCCTGCCAGTTCGGCTCTCTCTCC 460
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DB 761 CAGGAGACGCTGCACCGGTGTGACGCTGTGCACAGAGGATGTTAAGAGAGTTCGATC 820
QY 779 TCAGTGCAGGAGCGGAGGTGACAGACAGCA 809
DB 821 TCANTGCAGGAGCGGAGGTGACAGACAGCA 851

RESULT 3
LOCUS BY751423 692 bp mRNA linear EST 17-DEC-2002
DEFINITION BY751423 RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F830034B13 5', mRNA sequence.
ACCESSION BY751423
VERSION BY751423.1 GI:27181814
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 692)
AUTHORS Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Okazaki, Y., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Nikaido, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C. A.,
Hume, D. A., Quackenbush, J., Schram, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Belsel, K. W., Blake, J. A., Bratt, D., Bruscia, V.,
Cathala, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawachi, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochi, I. V., Lee, Y., Lenhard, S., Lyons, P. A., Maglott, D. R.,
Numata, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sardelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wanstedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wyszynski, B., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

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Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL  
MEDLINE  
PIUMED

COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Hirozane, T., Hori, F., Fukuda, S., Hashizume, W., Hayashida, K., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

# FEATURES

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# RESULT 6

BY751441

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY751441 RIKEN full-length enriched, activated spleen Mus musculus  
cDNA clone F830034K15 5', mRNA sequence.

BY751441.1 GI:27181840  
Mus musculus (house mouse)  
Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 665)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Buit, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, F., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takanaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

TITLE

JOURNAL





Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

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Location/Qualifiers  
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Matches 497; Conservative 0; Mismatches 7; Indels 25; Gaps 2;  
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## RESULT 9

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VERSION BF166137.1 GI:11046489  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 941)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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High quality sequence stop: 668.

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Query Match 55.0%; Score 444.6; DB 10; Length 941;  
Best Local Similarity 93.6%; Pred. No. 7.2e-125;  
Matches 495; Conservative 0; Mismatches 9; Indels 25; Gaps 2;  
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Db 29 ATGGTGTCTTTGCTCGGCTGTGGCGCTATGGGCTGCTTGTGACAGCGGTCCATCTA 88  
QY 61 GGGCAGTGTGTACGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120  
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QY 181 CCATGTGACTCAGGCGAATTTCTCAGCCAGTGGAAACAGGAGATTTCGCTGTCCAGCAC 240  
Db 208 CCATGTGACTCAGGCGAATTTCTCAGCCAGTGGAAACAGGAGATTTCGCTGTCCAGCAC 267  
QY 241 AGACACTGTGAAACCCAGTGGCTGGGCTGCTCGGAAAGGATCAAGGGCTTCGGGTTAAG 300  
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QY 361 AGCAAGGATTCGAGGATGCTGTCTCAGCACGCCCTGTATCCCTCGCTTGGAGTTATG 420
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DEFINITION BY745260 RIKEN full-length enriched, bone marrow macrophage Mus
musculus cDNA clone I830083B08 5', mRNA sequence.
ACCESSION BY745260
VERSION BY745260.1 GI:27172371
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS
Okazaki,Y., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Nikaido,I., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V.,
Ciothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmerond,S.,
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Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
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Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
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Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
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Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tsgami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken. Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues  
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

Location/Qualifiers  
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QY 1 ATGGTGCTTTTCCCTCGCGCTGTGCGCGCTATGGGGCTGTTGTTCAGACGGTCCATCTA 60  
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VERSION CB547441.1 GI:29431382
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SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 603)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00106 row: f column: 8.
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Matches 453; Conservative 0; Mismatches 64; Indels 24; Gaps 1;

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QY 241 AGACACTGTGAACCCAGTGCCTGGGGCTGCCTGGGAAGGATCAAGGCTTCGGGTTAAG 300
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cDNA clone F830006N20 5', mRNA sequence.
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VERSION BY211683.1 GI:26392288
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SOURCE Mus musculus (house mouse)
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 440)
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogama, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
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Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL 22354683
MEDLINE 12466851
PUBMED
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
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Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues  
Issues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC building Addenbrookes Hospital Cambridge) whose  
assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

## FEATURES

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SOURCE  
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ORGANISM

## REFERENCE

1 (Bases 1 to 435)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
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Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
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Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

## TITLE

## JOURNAL

22354683  
12466851  
Contact: Yoshihide Hayashizaki  
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Sciences Center (GSC), Yokohama Institute  
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Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
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Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

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Matches 405; Conservative 0; Mismatches 1; Indels 24; Gaps 1;  
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## RESULT 14

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DEFINITION BY211594 RIKEN full-length enriched, activated spleen Mus musculus  
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## REFERENCE

AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 429)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maizels, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
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Nature 420, 563-573 (2002)  
22354683  
12466851

## COMMENT

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Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
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## FEATURES

Location/Qualifiers  
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Shingawa, A., Yasunishi, A., and Yoshizaki, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
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Nature 420, 563-573 (2002)  
12354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Aizawa, K., Akimura, T., Arakawa, T.,  
Hiroyane, T., Imotani, K., Ishii, Y.,  
Miyazaki, A., Murata, N., Nakamura, M.,  
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Shiraki, T., Tagami, M., Waki, K.,  
Watahiki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
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RIKEN integrated sequence analysis (RISA) system--384-format  
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Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirotsawa, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

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QY 241 AGACACTGTGAACCCAGTGGTGGGCTGCCTGGGAAGGGATCAAGGGCTTCGGGTTAAG 300
Db |||||||||||||||
QY 310 AGACACTGTGAACCCA-----ATCAAGGGCTTCGGGTTAAG 345
Db |||||||||||||||
QY 301 AAGGAGGGCACCGCAGAAATCAGACACTGTGTACCTGTAAAGGAAGGACAACACTGCACCC 360
Db |||||||||||||||
QY 346 AAGGAGGGCACCGCAGAAATCAGACACTGTGTACCTGTAAAGGAAGGACAACACTGCACCC 405
Db |||||||||||||||
QY 361 AGCAAGGATTGCGAGGCATGTGCTCAGCACAGCCCTGTATCCCTGGCTTTGGAG 415
Db |||||||||||||||
QY 406 AGCAAGGATTGCGAGGCATGTGCTCAGCACAGCCCTGTATCCCTGNGCTTGGAG 460
Db |||||||||||||||
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Search completed: July 25, 2004, 01:47:41  
Job time : 2505 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 25, 2004, 00:43:22 ; Search time 3294 Seconds  
(without alignments)  
10644.965 Million cell updates/sec

Title: US-10-031-607-6  
Perfect score: 809  
Sequence: 1 atgggttttgcctcggt.....gggcaggtgacagacgca 809

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
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27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rtd.\*  
36: em\_htg\_nam.\*  
37: em\_htg\_vrt.\*  
38: em\_sv.\*  
39: em\_hcgo\_hum.\*  
40: em\_hcgo\_mus.\*  
41: em\_hcgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	809	100.0	809	6	AX077882	AX077882 Sequence
2	751	92.8	869	10	MMU401387	AJ401387 Mus muscu
3	742	91.7	776	6	AX077880	AX077880 Sequence
4	679	83.9	870	6	BD237352	BD237352 Improve
5	679	83.9	870	6	AX027014	AX027014 Sequence
6	679	83.9	1579	6	AX0708386	AX0708386 Sequence
7	679	83.9	1579	10	MUSCD40A	M83312 Mouse CD40
8	666.2	82.3	1281	10	BC029254	BC029254 Mus muscu
9	659	81.5	926	10	MMU401389	AJ401389 Mus muscu
10	623.8	77.1	844	10	MMU401390	AJ401390 Mus muscu
11	568	70.2	1032	10	MMU401388	AJ401388 Mus muscu
12	547	67.6	788	6	AX077881	AX077881 Sequence
13	429.2	53.1	934	6	AX077879	AX077879 Sequence
14	380.4	47.0	547	10	AF241231	AF241231 Rattus no
15	351.4	43.4	1114	6	AX780303	AX780303 Sequence
16	317.6	39.3	759	9	HSA300189	AJ300189 Homo sapi
17	312.8	38.7	469	6	AX708387	AX708387 Sequence
18	280.4	34.7	834	6	BD237349	BD237349 Improve
19	280.4	34.7	834	6	AX027007	AX027007 Sequence
20	280.4	34.7	910	6	AX823746	AX823746 Sequence
21	280.4	34.7	1004	6	AR138075	AR138075 Sequence
22	280.4	34.7	1004	6	AR153584	AR153584 Sequence
23	280.4	34.7	1004	6	BD250531	BD250531 Identific
24	280.4	34.7	1004	6	I07284	I07284 Sequence 31
25	280.4	34.7	1004	6	AR242452	AR242452 Sequence
26	280.4	34.7	1004	6	AR270724	AR270724 Sequence
27	280.4	34.7	1004	6	AR368347	AR368347 Sequence
28	280.4	34.7	1004	6	AR380717	AR380717 Sequence
29	280.4	34.7	1004	6	AX700827	AX700827 Sequence
30	280.4	34.7	1004	6	AX771495	AX771495 Sequence
31	280.4	34.7	1004	6	AX774954	AX774954 Sequence
32	280.4	34.7	1004	6	BD015196	BD015196 TLISA cel
33	280.4	34.7	1004	6	BD226626	BD226626 Antisense
34	280.4	34.7	1004	9	HSCDW40	X60592 Human CDw40
35	280.4	34.7	1157	9	BC012419	BC012419 Homo sapi
36	272.4	33.7	1004	6	BD268055	BD268055 Use of an
37	251.6	31.1	837	6	BD237354	BD237354 Improve
38	251.6	31.1	837	6	AX027018	AX027018 Sequence
39	249.6	30.9	741	6	AX781593	AX781593 Sequence
40	249.6	30.9	1126	6	AX077878	AX077878 Sequence
41	246.8	30.5	845	6	AX027450	AX027450 Sequence
42	246.8	30.5	1276	4	AF248545	AF248545 Sus scrof
43	240.4	29.7	1770	6	AX823728	AX823728 Sequence
44	230.6	28.5	669	9	AY225405	AY225405 Homo sapi
45	230.6	28.5	1088	6	AX823724	AX823724 Sequence

ALIGNMENTS

RESULT 1  
AX077882  
LOCUS AX077882 809 bp DNA linear PAT 22-FEB-2001  
DEFINITION Sequence 6 from Patent WO0105967.  
ACCESSION AX077882  
VERSION AX077882.1 GI:13157729  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Savitzky, K., Khosravi, R. and Elazar, M.  
TITLE Splice variants of cd40-receptor  
JOURNAL Patent: WO 0105967-A 6 25-JAN-2001;

Compugen Ltd. (IL)		Location/Qualifiers	
FEATURES	source	1. .809	
		/organism="Homo sapiens"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:9606"	
ORIGIN			
Query Match	100.0%;	Score 809;	DB 6; Length 809;
Best Local Similarity	100.0%;	Pred. No. 2.9e-244;	
Matches 809;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	ATGGTGCTTTGCCCTCGCGCTGCGCGCTATGGGGCTGCTTTGTTGACAGCGGTCCATCTA	60
DB	1	ATGGTGCTTTGCCCTCGCGCTGCGCGCTATGGGGCTGCTTTGTTGACAGCGGTCCATCTA	60
QY	61	GGGCAGTGTGTTACGTGTCAGTGACAAACAGTACTCTCCAGCATGCCAGTGCCTGTGATTG	120
DB	61	GGGCAGTGTGTTACGTGTCAGTGACAAACAGTACTCTCCAGCATGCCAGTGCCTGTGATTG	120
QY	121	TGCCAGCCAGGAAGCGACTGACAAAGCCACTGTCACAGCTCTTTGAGAGACCCGATGCCAC	180
DB	121	TGCCAGCCAGGAAGCGACTGACAAAGCCACTGTCACAGCTCTTTGAGAGACCCGATGCCAC	180
QY	181	CCATGTGACTCAGCGGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCACACGAC	240
DB	181	CCATGTGACTCAGCGGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCACACGAC	240
QY	241	AGACACTGTGAACCCAGTGCCTGGGGCTGCTGGGAGGGATCAAGGCTTCGGGTTAAG	300
DB	241	AGACACTGTGAACCCAGTGCCTGGGGCTGCTGGGAGGGATCAAGGCTTCGGGTTAAG	300
QY	301	AAGGAGGGCACCAGATTCAGTGTGCTGCTGACAGCCGCTGTATCCCTGGCTTGGAGTTATG	360
DB	301	AAGGAGGGCACCAGATTCAGTGTGCTGCTGACAGCCGCTGTATCCCTGGCTTGGAGTTATG	360
QY	361	AGCAAGGATTCGAGGATGTGCTCAGACAGCCGCTGTATCCCTGGCTTGGAGTTATG	420
DB	361	AGCAAGGATTCGAGGATGTGCTCAGACAGCCGCTGTATCCCTGGCTTGGAGTTATG	420
QY	421	GAGATGCCACTGAGACACTGATACCGTCTGTATCCCTGCCAGTCGCTTCTTCTCC	480
DB	421	GAGATGCCACTGAGACACTGATACCGTCTGTATCCCTGCCAGTCGCTTCTTCTCC	480
QY	481	AATCAGTCACTATTTTCGAAAAGTGTATCCCTGGCAAAAGTAAAGTCCCGATGCG	540
DB	481	AATCAGTCACTATTTTCGAAAAGTGTATCCCTGGCAAAAGTAAAGTCCCGATGCG	540
QY	541	AGCCCTGTGTCATCTCTGTGATGGGCACTCCTCATCACCATTTCGGGGTGTTC	600
DB	541	AGCCCTGTGTCATCTCTGTGATGGGCACTCCTCATCACCATTTCGGGGTGTTC	600
QY	601	CTATATCAAAAAGTGGTCAAGAACCAAGGATAATGAGATGTTACCCCTCGGGCTCG	660
DB	601	CTATATCAAAAAGTGGTCAAGAACCAAGGATAATGAGATGTTACCCCTCGGGCTCG	660
QY	661	ACGGCAAGATCCCAGAGATGGAAGATTATCCCGGTATAACACCGCTGTCCAGTGCA	720
DB	661	ACGGCAAGATCCCAGAGATGGAAGATTATCCCGGTATAACACCGCTGTCCAGTGCA	720
QY	721	GGAGACACTGCACGGGTGTACGCTGTGTCACAGGAGGATGTTAAAGAGAGTCGATCTC	780
DB	721	GGAGACACTGCACGGGTGTGCTGTCACAGGAGGATGTTAAAGAGAGTCGATCTC	780
QY	781	AGTGAGGAGCGCGAGTGCACAGCA	809
DB	781	AGTGAGGAGCGCGAGTGCACAGCA	809

AJ401387		GI:13016729	
VERSION	AJ401387.1	GI:13016729	
KEYWORDS	alternative splicing; CD40 gene; CD40 type II isoform.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1	Tone, M., Tone, Y., Fairchild, P.J., Wykes, M. and Waldmann, H. Regulation of CD40 function by its isoforms generated through alternative splicing	
AUTHORS	2	Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)	
TITLE	21117110		
JOURNAL	11172023		
MEDLINE	11172023		
PUBMED	11172023		
REFERENCE	2	(bases 1 to 869)	
AUTHORS	Tone, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JUL-2000)	Tone M., Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE	
UNITED KINGDOM			
Location/Qualifiers			
FEATURES	source	1. .869	
		/organism="Mus musculus"	
		/mol_type="mRNA"	
		/db_xref="taxon:10090"	
gene	1. .869		
CDS	7. .618		
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		/db_xref="GI:13016730"	
		/db_xref="GOA:P27512"	
		/db_xref="SWISS-PROT:P27512"	
		/translation="MVSFLRLCALWGGCLLTAHLGQCVTCDSKQYLHDGQCDLCPQF SRLTSHCTALEKTCQPCDSGEFAOWNREIRCHQHRCEPNQGLRVKKEGTAESTDV CTCKEGQCTSKDCEACAOHTPCIPGFGVMEMATEITDTVTCHFCPVGFNFQNSLFEK CYPTRFKVPDASPAGHSRCDHPHHFRGVSLYQKGGQETKG"	
ORIGIN			
Query Match	92.8%;	Score 751;	DB 10; Length 869;
Best Local Similarity	97.0%;	Pred. No. 6.7e-226;	
Matches 785;	Conservative 0;	Mismatches 0;	Indels 24; Gaps 1;
QY	1	ATGGTGCTTTTGCCTCGGCTGTGGCGCTATGGGCTGCTTGTTCAGACGGTCCATCTA	60
DB	7	ATGGTGCTTTTGCCTCGGCTGTGGCGCTATGGGCTGCTTGTTCAGACGGTCCATCTA	66
QY	61	GGGCAGTGTGTTACGTGTCAGTGACAAACAGTACTCCACGATGCCAGTGTGTGATTG	120
DB	67	GGGCAGTGTGTTACGTGTCAGTGACAAACAGTACTCCACGATGCCAGTGTGTGATTG	126
QY	121	TGCCAGCCAGGAAGCGGACTGACAGCCACTGTCACAGCTCTTGAGAGACCCGATGCCAC	180
DB	127	TGCCAGCCAGGAAGCGGACTGACAGCCACTGTCACAGCTCTTGAGAGACCCGATGCCAC	186
QY	181	CCATGTGACTCAGGCGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCCAGCAC	240
DB	187	CCATGTGACTCAGGCGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCCAGCAC	246
QY	241	AGACACTGTGAACCCAGTGCCTGGGAGGATCAAGGCTTCGGGTTAAG	300
DB	247	AGACACTGTGAACCCA-----ATCAAGGCTTCGGGTTAAG	282
QY	301	AAGGAGGGCACCAGAGAAATCAGACACTGCTGTACTCTGAAGGAGGACAACTGCAC	360
DB	283	AAGGAGGGCACCAGAGAAATCAGACACTGCTGTACTCTGAAGGAGGACAACTGCAC	342
QY	361	AGCAAGGATTCGAGGCAATGCTCAGACACGCTGTATCCCTGGCTTGGAGTTATG	420
DB	343	AGCAAGGATTCGAGGCAATGCTCAGACACGCTGTATCCCTGGCTTGGAGTTATG	402

RESULT 2

MMU401387

LOCUS

DEFINITION

Mus musculus mRNA for CD40 type II isoform (CD40 gene), ROD 01-JUN-2001

linear

mRNA

869 bp

Mus musculus

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## gene

## CDS

## Location/Qualifiers

## 1. .869

## /organism="Mus musculus"

## /mol\_type="mRNA"

## /db\_xref="taxon:10090"

## 1. .869

## /gene="CD40"

## 7. .618

## /gene="CD40"

## /note="alternative transcript"

## /codon\_start=1

## /product="CD40 type II isoform"

## /protein\_id="CAC29427.1"

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## /db\_xref="GOA:P27512"

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## /translation="WSLPLCALWGGLTAVHLGQCVTCSDKQYLHGGCCDL-CORG

## SRLTSHCTALEKTQCHPCDSGFSAQWNRREIRCHQHRCEPNQGLRVKRGTAESDVI

## CTCKEGQHCCTKCEACATPCTPGFVGMEMATEITDITVCHPCPVGFFSNQSLFEK

## CYPWTRFKVPDASPAGHSCRDGPHHFRGVSLYQKGQETKG"

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## 0; Mismatches

## 0; Indels

## 24; Gaps

## 1;

## QY

## Db

## QY

## Db

## QY

## Db

## QY

## Db

## QY

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## QY

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## Db





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QY 719 CAGGAGACACTGCACGGGTGTGAGCCTGTGCACACAGGAGGATGGTAAAGAGAGTGGCATC 778
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QY 779 TCAGTGCAGAGCGGCGCAGGTGACAGACGA 809
Db 817 TCAGTGCAGAGCGGCGCAGGTGACAGACGA 847

RESULT 6
AX708386
LOCUS AX708386 1579 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 17 from Patent WO02061135.
ACCESSION AX708386
VERSION AX708386.1 GI:29564273
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Lorenz, M.
TITLE Dna array sequence selection
JOURNAL Patent: WO 02061135-A 17 08-AUG-2002;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN
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Best Local Similarity 90.1%; Pred. No. 4.4e-203;
Matches 785; Conservative 0; Mismatches 0; Indels 86; Gaps 2;
QY 1 ATGGTGTCTTTGCTCGGCTGTGCGGCTATGGGCTGCTTTCACAGCGGTGCATCTA 60
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QY 61 GGGCAGTGTGTACGTGCAGTGAACAAAGTACCTCCACAGTGGCAGGTGTGATTG 120
Db 69 GGGCAGTGTGTACGTGCAGTGAACAAAGTACCTCCACAGTGGCAGGTGTGATTG 128
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Db 129 TGCCAGCCAGGAAGCGGCTGACAGCCACTGACAGCTCTTGAGAAGACCAATGCCAC 188
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QY 241 AGACACTGTGAACCCAGTGGCTGGGCTGCCCTGGGAGGATCAAGGGCTTCGGTTAAG 300
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QY 301 AAGAGGGGACCCGAGAAATCAGACACTGCTGTACTGTAAAGAAAGGACCACTGCGACC 360
Db 285 AAGAGGGGACCCGAGAAATCAGACACTGCTGTACTGTAAAGAAAGGACCACTGCGACC 344
QY 361 AGCAAGGATTCGAGGCATGTGCTAGCAGCAGCCCTGTATCCCTGGCTTTGGAGTTATG 420
Db 345 AGCAAGGATTCGAGGCATGTGCTAGCAGCAGCCCTGTATCCCTGGCTTTGGAGTTATG 404
QY 421 GAGATGGCCACTGAGACCACTGATACCGCTGTCTATCCCTGCCAGTGGCTTCTTCTCC 480
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Db 765 CAGGAGACACTGCACGGGTGTGACGCTGTGCACACAGGAGGATGTTAAGAGAGTTCGATC 824
QY 779 TCAGTGCAGGAGCGGCGCAGGTGACAGACGA 809
Db 825 TCAGTGCAGGAGCGGCGCAGGTGACAGACGA 855

RESULT 7
MUSCD40A
LOCUS MUSCD40A 1579 bp mRNA linear ROD 23-SEP-1996
DEFINITION Mouse CD40 mRNA, complete cds.
ACCESSION M83312
VERSION M83312.1 GI:1853058
KEYWORDS CD40 antigen.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1579)
TITLE Differential increase of an alternatively polyadenylated mRNA
JOURNAL species of murine CD40 upon B lymphocyte activation
MEDLINE J. Immunol. 148 (2), 620-626 (1992)
PUBMED 92105763
REFERENCE 2 (bases 1 to 1579)
AUTHORS Grimaldi, J.C., Torres, R., Kozak, C.A., Chang, R., Clark, E.A.,
Howard, M. and Cockayne, D.A.
TITLE Genomic structure and chromosomal mapping of the murine CD40 gene
MEDLINE J. Immunol. 149 (12), 3921-3926 (1992)
PUBMED 93094586
REFERENCE 3 (bases 1 to 1579)
AUTHORS Torres, R.M.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1996) Raul M. Torres, Basel Institute for
Immunology, Basel, CH-4005, Switzerland
COMMENT On Sep 23, 1996 this sequence version replaced gi:192519.
FEATURES
source Location/Qualifiers
1..1579
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1..1579
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9..878
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/db_xref="GI:1553059"
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arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMV. "

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/lab\_host="DH105"

/note="Vector: pCMV-Sport6"

1. .1281

/gene="Tnfrsf5"

/note="synonyms: IGM, p50, Bp50, GP39, IMD3, TRAP, HIGM1, T-BAM"

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31. .900

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/db\_xref="LocusID:21939"

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343. .459

/note="TNFR; Region: Tumor necrosis factor receptor / nerve growth factor receptor repeats. Repeats in growth factor receptors that are involved in growth factor binding. TNF/TNFR"

/db\_xref="CDD:smart00208"

ORIGIN

Query Match 82.3%; Score 666.2; DB 10; Length 1281;

Best Local Similarity 89.2%; Pred. No. 4.9e-199;

Matches 777; Conservative 0; Mismatches 8; Indels 86; Gaps 2;

QY 1 ATGGTGCTTTGCTCGGCTGCGCGCTATGGGCTGCTTGTACAGCGGTCCATCTA 60

DB 31 ATGGTGCTTTGCTCGGCTGCGCGCTATGGGCTGCTTGTACAGCGGTCCATCTA 90

QY 61 GGGAGTGTGTACGTGAGTGAACAAAGTACCTCCAGATGGCGAGTGTGTGATTG 120

DB 91 GGGAGTGTGTACGTGAGTGAACAAAGTACCTCCAGATGGCGAGTGTGTGATTG 150

QY 121 TGCACCGAGGAGCGGCTGACAGCCACTGCAGAGCTTTGAGAAGACCAATGCCAC 180

DB 151 TGCACCGGAGAGCGGCTGACAGCCACTGCAGAGCTTTGAGAAGACCAATGCCAC 210

QY 181 CCATGTGACTCAGGCGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCCACGAC 240

DB 211 CCATGTGACTCAGGCGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCCACGAC 270

QY 241 AGACACTGTGAACCGAGTGGTGGGCTGCTGGGAGGATCAAGGCTTCGGGTAA 300

DB 271 AGACACTGTGAACCGA-----ATCAAGGGCTTCGGGTAA 306

QY 301 AAGAGGGCACCAGCAATCAGACACTGTCTGTACCTGTAAAGAGGAGCAACACTGCAC 360

DB 307 AAGAGGGCACCAGCAATCAGACACTGTCTGTCTGTAAAGAGGAGCAACACTGTAC 366

QY 361 AGCAAGATTGGAGGATGTCTCAGACAGCGCTGTATCCCTGGCTTGGAGTTATG 420

DB 367 AGCAAGATTGGAGGATGTCTCAGACAGCGCTGTATCCCTGGCTTGGAGTTATG 426

QY 421 GAGATGGCACTGAGACCACTGATACCGTGTCTATCCCTGCCAGTGGCTTCTTCC 480

DB 427 GAGATGGCACTGAGACCACTGATACCGTGTCTATCCCTGCCAGTGGCTTCTTCC 486

QY 481 AATCAGTCATCACTTTTCGAAAAGTGTATCCCTGGACAA----- 520

DB 487 AATCAGTCATCACTTTTCGAAAAGTGTATCCCTGGACAAAGCTGTGAGGATAAGAACTG 546

QY 521 -----GGTTTAAGTCCCGGATG 538

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QY 539 CGAGCCCTGCTGCTCATCTCTGTCGTCGTCATCTCATCACCATTTCGGGGTGT 598

DB 607 CGAGCCCTGCTGCTCATCTCTGTCGTCGTCATCTCATCACCATTTCGGGGTGT 666

QY 599 CTCTATATCAAAAGGTGTCACAGAAACCAAGAGTAATGAGATGTTACCCCTCGCGCT 658

DB 667 CTCTATATCAAAAGGTGTCACAGAAACCAAGAGTAATGAGATGTTACCCCTCGCGCT 726

QY 659 CGAGGCAAGATCCCGAGGAGTGGAGATTATCCCGTTCATACACCGCTGCTCCAGTG 718

DB 727 CGAGGCAAGATCCCGAGGAGTGGAGATTATCCCGTTCATACACCGCTGCTCCAGTG 786

QY 719 CAGGAGACACTGCACGGGTGTTCAGCCCTGTCCACAGAGGAGTGGTAAAGAGATCGCATC 778

DB 787 CAGGAGACGCTGCACGGGTGTTCAGCCCTGTCCACAGAGGAGTGGTAAAGAGATCGCATC 846

QY 779 TCAGTCAGGAGCGGCGAGGTGCACAGACGCA 809

DB 847 TCAGTCAGGAGCGGCGAGGTGCACAGACGCA 877

RESULT 9

MMU401389

LOCUS Mus musculus mRNA for CD40 type IV isoform (CD40 gene). 926 bp mRNA linear ROD 01-JUN-2001

DEFINITION Mus musculus mRNA for CD40 type IV isoform (CD40 gene).

ACCESSION AJ401389

VERSION AJ401389.1 GI:13016733

KEYWORDS alternative splicing; CD40 gene; CD40 type IV isoform.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

REFERENCE

AUTHORS Tone, M., Tone, Y., Fairchild, P.J., Wykes, M. and Waldmann, H.

TITLE Regulation of CD40 function by its isoforms generated through alternative splicing

JOURNAL Proc Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)

MEDLINE 21117110

PUBMED 11172023

REFERENCE 2 (bases 1 to 926)

AUTHORS Tone, M.

TITLE Direct Submission

JOURNAL Submitted (19-JUL-2000) Tone M., Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE, UNITED KINGDOM

FEATURES

Location/Qualifiers

1. .926

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

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/gene="CD40"

7. .675

/gene="CD40"

/note="alternative transcript"

/codon\_start=1

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/db\_xref="GI:13016734"

/db\_xref="GOA:P27512"

/db\_xref="SWISS-PROT:P27512"

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ORIGIN

Query Match 81.5%; Score 659; DB 10; Length 926;

Best Local Similarity 89.6%; Pred. No. 8.9e-197;

Matches 780; Conservative 0; Mismatches 0; Indels 91; Gaps 3;



Db 463 AATCAGTCATCACTTTTCGAAAGGTTATCCCTGGACAAGCTGTGAGGATAAGAA----- 518  
Qy 541 AGCCCTGCTGTCATCTCTGTCGATGGGATCTCTATCACCATTTCGGGGTGTTCCT 600  
Db 519 -----CTTGAGGCTCTCAGAAAGGAACAGATCAGATCAATGT 557  
Qy 601 CPATATCAAAAAGGTGGTCAAGAAACCAAGGATTAATGAGATGTTACCCCTGCGGCTCG 660  
Db 558 CATCTGTGAAGAGTGGTCAAGAAACCAAGGATTAATGAGATGTTACCCCTGCGGCTCG 617  
Qy 661 AGCGAAGATCCCGAGGAGATGAAGATTAATCCCGGTATTAACACCGTGTCTCAGTGCA 720  
Db 618 AGCGAAGATCCCGAGGAGATGAAGATTAATCCCGGTATTAACACCGTGTCTCAGTGCA 677  
Qy 721 GGAGACATGTCACGGGTGTCAGCCTGTACACAGAGGATGTTAAAGAGATCGCATCTC 780  
Db 678 GGAGACATGTCACGGGTGTCAGCCTGTACACAGAGGATGTTAAAGAGATCGCATCTC 737  
Qy 781 AGTCAGGAGCGCAGGTGACAGACGCA 809  
Db 738 AGTCAGGAGCGCAGGTGACAGACGCA 766

## RESULT 11

MMU401388 1032 bp mRNA linear ROD 01-JUN-2001  
LOCUS Mus musculus mRNA for CD40 type III isoform (CD40 gene).  
DEFINITION AJ401388  
VERSION AJ401388.1 GI:13016731  
KEYWORDS alternative splicing; CD40 gene; CD40 type III isoform.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE Tone, M., Tone, Y., Fairchild, P.J., Wykes, M. and Waldmann, H.  
Regulation of CD40 function by its isoforms generated through  
alternative splicing  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)  
MEDLINE 21117110  
PUBMED 11172023  
REFERENCE 2 (bases 1 to 1032)  
AUTHORS Tone, M.  
TITLE Direct Submission  
JOURNAL Submitted (19-JUL-2000) Tone M., Sir William Dunn School of  
Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE,  
UNITED KINGDOM

## FEATURES

Location/Qualifiers

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/organism="Mus musculus"  
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CDS 7..711  
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## ORIGIN

Query Match 70.2%; Score 568; DB 10; Length 1032;  
Best Local Similarity 80.8%; Pred. No. 5.8e-168;

RESULT 12  
AX077881

Matches 785; Conservative 0; Mismatches 0; Indels 187; Gaps 3;  
Qy 1 ATGGTGTCTTTGCTCGGCTGTGGCGCTATGGGCTGTGTTGACAGCGGTCCATCTA 60  
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Qy 61 GGGCAGTGTGTTACGTGACGTGACAAACAGTACTCTCCAGATGGCCAGTCTGTGATTG 120  
Db 67 GGGCAGTGTGTTACGTGACGTGACAAACAGTACTCTCCAGATGGCCAGTCTGTGATTG 126  
Qy 121 TGCAGCCAGGAGCGCACTGACAGCCACTGCACAGCTCTTTCAGAGAGCCCAATGCCAC 180  
Db 127 TGCAGCCAGGAGCGCACTGACAGCCACTGCACAGCTCTTTCAGAGAGCCCAATGCCAC 186  
Qy 181 CCATGTCACTCAGCGCAATTTCTCAGCCCACTGAGAAAGGAGAGATTGCTGTCCACAGCAC 240  
Db 187 CCATGTCACTCAGCGCAATTTCTCAGCCCACTGAGAAAGGAGAGATTGCTGTCCACAGCAC 246  
Qy 241 AGACACTGTGAACCCAGTGTGGGGTGTGGGAGGAGATCAAGGGCTTCGGGTTAAG 300  
Db 247 AGACACTGTGAACCCA-----ATCAAGGGCTTCGGGTTAAG 282  
Qy 301 AAGGAGGGCACCGCAGAAATCAGACACTGTCTGTACCTGTAAAGGAAGACAACTGCACC 360  
Db 283 AAGGAGGGCACCGCAGAAATCAGACACTGTCTGTACCTGTAAAGGAAGACAACTGCACC 342  
Qy 361 AGCAAGATTGCGAGGATGTGTCTGACACACGCGCTGTATCCCTGCTTGGAGTTATG 420  
Db 343 AGCAAGATTGCGAGGATGTGTCTGACACACGCGCTGTATCCCTGCTTGGAGTTATG 402  
Qy 421 GAGATGCCACTGAGACCACTGATACCGTCTGTATCCCTGCCAGTCGCTTCTCTCC 480  
Db 403 GAGATGCCACTGAGACCACTGATACCGTCTGTATCCCTGCCAGTCGCTTCTCTCC 462  
Qy 481 AATCAGTCATCACTTTTCGAAAAGTGTATCCCTCGGACAA----- 520  
Db 463 AATCAGTCATCACTTTTCGAAAAGTGTATCCCTCGGACAAAGCTGTGAGGATAAGAACTTG 522  
Qy 521 -----GGTTTAAAGTCCCGATG 538  
Db 523 GAGTCTCTACAGAAAGAACAGATCAGATTAATGTATCTGTGGTTTAAAGTCCCGATG 582  
Qy 539 CGAGCCCTGTGTGTCATCTCTGTCGTCATGGGATCTCATCACCATTTCGGGGTGTGT 598  
Db 583 CGAGCCCTGTGTGTCATCTCTGTCGTCATGGGATCTCATCACCATTTCGGGGTGTGT 642  
Qy 599 CTCTATATCA----- 608  
Db 643 CTCTATATCACTGAGTGTCTCAGGAGGAAAGGAGGAGGAGGTTACGCCCTGTGCAACCA 702  
Qy 609 -----AAAAAGTGG 617  
Db 703 GCCTCTGACTCACCTCGCAATGTCCCAACCCCTTCTTCTTCTCACTAGAAAAGTGG 762  
Qy 618 TCAAGAAACCAAGGATTAATGAGATGTTACCCCTGCGGTGCGACGCAAGATCCCGAG 677  
Db 763 TCAAGAAACCAAGGATTAATGAGATGTTACCCCTGCGGTGCGACGCAAGATCCCGAG 822  
Qy 678 AGATGGAAGATTATCCCGGTCTAATACACCGCTGTCCAGTGCAGGAGACACTGCACGGT 737  
Db 823 AGATGGAAGATTATCCCGGTCTAATACACCGCTGTCCAGTGCAGGAGACACTGCACGGT 882  
Qy 738 GTCAAGCTGTCTCAGCAGGAGGATGTTAAAGAGAGTTCGCATCTCAGTGCAGGAGCGGAG 797  
Db 883 GTCAAGCTGTCTCAGCAGGAGGATGTTAAAGAGAGTTCGCATCTCAGTGCAGGAGCGGAG 942  
Qy 798 TGACAGACAGCA 809  
Db 943 TGACAGACAGCA 954

LOCUS AX077881 788 bp DNA linear PAT 22-FEB-2001  
 DEFINITION Sequence 5 from Patent WO0105967.  
 ACCESSION AX077881  
 VERSION AX077881.1 GI:13157728  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Savitzky, K., Khosravi, R. and Elazar, M.  
 TITLE Splice variants of cd40-receptor  
 JOURNAL Patent: WO 0105967-A 5 25-JAN-2001;  
 Compugen Ltd. (IL)  
 FEATURES  
 Location/Qualifiers  
 source 1..788  
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 ORIGIN  
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 Best Local Similarity 95.3%; Pred. No. 2.5e-161;  
 Matches 584; Conservative 0; Mismatches 5; Indels 24; Gaps 1;  
 QY 1 ATGTGTCTTTGCTCGCTGTGGCGCTATGGGCTGTGTGTGACAGCGTCCATCTA 60  
 Db 1 ATGTGTCTTTGCTCGCTGTGGCGCTATGGGCTGTGTGTGACAGCGTCCATCTA 60  
 QY 61 GGGCAGTGTGTACCTGCAGTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
 Db 61 GGGCAGTGTGTACCTGCAGTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
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 Db 241 AGACACTGTGAACCCA-----ATCAAGGGCTTCGGGTTAAG 276  
 QY 301 AAGAGGGCACCGCAGAAATCAGACACTGTCTGTACCTGTAGGAGAGACACACTGCACC 360  
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 QY 361 AGCAAGGATTGCGAGGATGTGTGACACACCGCCCTGTATCCCTGGCTTTGGAGTTATG 420  
 Db 337 AGCAAGGATTGCGAGGATGTGTGACACACCGCCCTGTATCCCTGGCTTTGGAGTTATG 396  
 QY 421 GAGATGCCCACTGAGACCACTGATACCGTGTGTATCCCTGCCAGTTCCTCTCC 480  
 Db 397 GAGATGCCCACTGAGACCACTGATACCGTGTGTATCCCTGCCAGTTCCTCTCC 456  
 QY 481 AATCAGTCACTCACTTTTCGAAAGAGTTATCCCTGGCAAGGTTTAAAGTCCCGGATGCG 540  
 Db 457 AATCAGTCACTCACTTTTCGAAAGAGTTATCCCTGGCAAGGTTTAAAGTCCCGGATGCG 516  
 QY 541 AGCCCTGCTGGTCAATTCCTGTGTGATGGGATCCTCATCACCATTTCGGGGTGTCT 600  
 Db 517 AGCCCTGCTGGTCAATTCCTGTGTGATGGGATCCTCATCACCATTTCGGGGTGTCT 576  
 QY 601 CTATATCAAAAAG 613  
 Db 577 CTATATCAGTGAG 589

RESULT 13  
 AX077879 934 bp DNA linear PAT 22-FEB-2001  
 LOCUS  
 DEFINITION Rattus norvegicus CD40 protein mRNA, partial cds.

DEFINITION Sequence 3 from Patent WO0105967.  
 ACCESSION AX077879  
 VERSION AX077879.1 GI:13157726  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Savitzky, K., Khosravi, R. and Elazar, M.  
 TITLE Splice variants of cd40-receptor  
 JOURNAL Patent: WO 0105967-A 3 25-JAN-2001;  
 Compugen Ltd. (IL)  
 FEATURES  
 Location/Qualifiers  
 source 1..934  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 53.1%; Score 429.2; DB 6; Length 934;  
 Best Local Similarity 84.5%; Pred. No. 4.9e-124;  
 Matches 541; Conservative 0; Mismatches 43; Indels 56; Gaps 3;  
 QY 1 ATGTGTCTTTGCTCGCTGTGGCGCTATGGGCTGTGTGTGACAGCGTCCATCTA 60  
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 QY 61 GGGCAGTGTGTACCTGCAGTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
 Db 93 GGGCAGTGTGTACCTGCAGTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTG 152  
 QY 121 TGCAGCCAGAGACCGAGTGAACAGCACTGACAGCTTTGAGAGAGACCAATGCCAC 180  
 Db 153 TGCAGCCAGAGACCGAGTGAACAGCACTGACAGCTTTGAGAGAGACCAATGCCAC 212  
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 QY 241 AGACACTGTGAACCCAGTGTGGGGTGCCTCGGAGGGATCAAGGGCTTCGGGTTAAG 300  
 Db 273 AGACACTGTGAACCCA-----ATCAAGGGCTTCGGGTTAAG 308  
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 QY 541 AGCCCTGCTGGTCAATTCCTGTGTGATGGGATCCTCATCACCATTTCGGGGTGTCT 600  
 Db 517 AGCCCTGCTGGTCAATTCCTGTGTGATGGGATCCTCATCACCATTTCGGGGTGTCT 576  
 QY 601 CTATATCAAAAAGTGTGAGAAACCAAGGATAATGAG 640  
 Db 577 CTATATCAAAAAGTGTGAGAAACCAAGGATCTCGAG 616

RESULT 14  
 AF241231 547 bp mRNA linear ROD 22-MAR-2001  
 LOCUS  
 DEFINITION Rattus norvegicus CD40 protein mRNA, partial cds.

AF241231  
 AF241231.2 GI:13400107  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus  
 1 (bases 225 to 547)  
 Krzesz.R., Wagner.A.H., Cattaruzza,M. and Hecker,M.  
 Cytokine-inducible CD40 gene expression in vascular smooth muscle  
 cells is mediated by nuclear factor kappaB and signal transducer  
 and activation of transcription-1  
 FEBS Lett. 453 (1-2), 191-196 (1999)  
 99330195  
 PUBMED  
 10403401  
 2 (bases 225 to 547)  
 Krzesz.R. and Hecker.M.  
 Direct Submission  
 TITLE  
 Submitted (02-MAR-2000) Dept. of Cardiovascular Physiology, Univ.  
 of Goettingen, Humboldtallee 23, Goettingen 37073, Germany  
 3 (bases 1 to 547)  
 Gao.D. and Hecker.M.  
 Direct Submission  
 TITLE  
 Submitted (21-MAR-2001) Dept. of Cardiovascular Physiology, Univ.  
 of Goettingen, Humboldtallee 23, Goettingen 37073, Germany  
 Sequence update by submitter  
 On Mar 21, 2001 this sequence version replaced gi:7248905.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="Wistar"  
 /db\_xref="taxon:10116"  
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 ORIGIN  
 Query Match 47.0%; Score 380.4; DB 10; Length 547;  
 Best Local Similarity 84.7%; Pred. No. 1.3e-108;  
 Matches 448; Conservative 0; Mismatches 57; Indels 24; Gaps 1;  
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 DB 41 ATGCTGCCTTTGGCTCAGCTGTGGCGCTCTGGGGCTGTGTTGACAGCGTCCATCTA 100  
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 DB 101 GGACAGTGTGTACGTGACAGTCAACAGTACCTCCAGATGGCCAGTGTGTGATTG 160  
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 QY 241 AGACACTGTGAACCCAGTGTGGGGCTGCCTGGGAAGGAGATCAAGGGCTTCGGGTAAAG 300  
 DB 281 CGACACTGCGAATCTA-----ATCAAGGGCTTCAGGTAAAG 316  
 QY 301 AAGAGGGACCGCAGAAATCAGACACTGTCTGTACTGTAAAGAGGACAACTGACAC 360  
 DB 317 AAGAGGGACCGCGTNTCAGACACTGTTGTACCTGTGACAGGAGGAGGAGGAGTGC 376

QY 361 AGCAAGATTGCGAGGCAATGTCTCAGCACACAGCCCTGTATCCCTGGCTTTGGATTATG 420  
 DB 377 AGCAAGAGTGGAGACGTGGCTCAGCACAGAGCCCTGTGGCCTTTGGAGTCGTG 436  
 QY 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTCTCATCCCTGCCAGTCGGCTTCTTCTCC 480  
 DB 437 CAGATGGCCACTGAGACTACTGATACCGTCTGCCAACCTGCCGGTTCGGATTCTTCTCC 496  
 QY 481 AATCAGTCAATCACTTTTCGAAAAGTGTATCCCTCGCAAGGTTTAAAG 529  
 DB 497 AATGGGTCAATCACTTTTGAAGAGTGTATCCATCCATGGACAAGCTGTGAAG 545  
 RESULT 15  
 AX780303  
 LOCUS AX780303 1114 bp DNA linear PAT 14-JUL-2003  
 DEFINITION Sequence 2460 from Patent WO03039443.  
 ACCESSION AX780303  
 VERSION AX780303.1 GI:32697297  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1  
 AUTHORS Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,  
 Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.  
 TITLE Novel genetic markers for leukemias  
 JOURNAL Patent: WO 03039443-A 2460 15-MAY-2003;  
 Deutsches Krebsforschungszentrum (DE);  
 Ludwig-Maximilian-Universitaet Muenchen (DE);  
 PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)  
 FEATURES  
 Location/Qualifiers  
 1..1114  
 source /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 43.4%; Score 351.4; DB 6; Length 1114;  
 Best Local Similarity 67.5%; Pred. No. 2.1e-99;  
 Matches 537; Conservative 0; Mismatches 232; Indels 27; Gaps 2;  
 QY 1 ATGGTGCTTTGCTCGGCTGTGGCGCTATGGGGCTGTGTTGACAGCGTCCATCTA 60  
 DB 29 ATGGTTCGTCTCGCTCTGCAGTGGCTCTCTCTGGGGCTGTGTTGACCGGTGCCATCCA 88  
 QY 61 GGGCAGTGTGTACGTGACAGTCAAAACAGTACCTCCACGATGGCCAGTGTGTGATTG 120  
 DB 89 GAACACCCACTGTGATGCAGAGAAAAACAGTACCTAATAAACAGTCACTGCTGTCTTTG 148  
 QY 121 TGCCAGCGAGGAGCGCAGTCAACAGCCACTGACAGCTCTTTGAGAAGACCCAAATGCCAC 180  
 DB 149 TGCCAGCGCAGGACAGAAACTGGTGAAGTACTGCACAGAGTTCACTGAAACGGATGCTT 208  
 QY 181 CCATGTGACTCAGCGAATCTCAGCCAGTGGAGAGGAGATTCGCTGTCCACAGCAC 240  
 DB 209 CTTTGGCGTGAAGCGAATTCCTAGACACCTGGAAACAGAGACACACTGCCACAGCAC 268  
 QY 241 AGACACTGTGAACCCAGTGTGGGGCTGCCTGGGAAGGAGATCAAGGGCTTCGGGTAAAG 300  
 DB 269 AAATCTCGGACCCCA-----ACCTAGGGCTTCGGGTCCAG 304  
 QY 301 AAGAGGGACCGCAGAAATCAGACACTGTGTGTACTGTAAAGAGGAGACAACTGACAC 360  
 DB 305 CAGAAGGGCACCTCAGAAACAGACACCATCTGCACTGTGAAGAAGGCTGGCACTGTACG 364  
 QY 361 AGCAGGATTGCGAGGCAATGCTCAGCACACCGCCCTGTATCCCTGGCTTTGGAGTTATG 420  
 DB 365 AGTGAGGCTGTAGAGCTGTCTCTGACCGCTATGCTGCGCCGGCTTTGGGGTCAAG 424  
 QY 421 GAGATGGCCACTGAGACCACTGATACCGTGTGTATCCCTGTCCAGTGGCTTCTTCTCC 480



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OM protein - protein search, using sw model

Run on: July 21, 2004, 10:03:39 ; Search time 16 Seconds  
(without alignments)  
961.915 Million cell updates/sec

Title: US-10-031-607-7

Perfect score: 913  
Sequence: 1 MVRPLQCVLMGCLLTAVHP.....WLCNRQAQTRMLSVVPRIG 160

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	785	86.0	277	2 A60771	B-cell activation
2	483	52.9	305	2 A46476	B cell-associated
3	212.5	23.3	461	1 A33356	tumor necrosis fac
4	200	21.9	435	2 I54182	tumor necrosis fac
5	188.5	20.6	324	2 JC2395	Fas antigen precu
6	180	19.7	327	2 A46484	apoptosis-mediati
7	174.5	19.1	459	2 I48854	gene murine tumou
8	173	18.9	474	2 B38634	tumor necrosis fac
9	170	18.6	349	2 D72175	G2R protein - vari
10	170	18.6	349	2 D38858	gene GAR protein -
11	167.5	18.3	260	1 A45117	CD27 antigen precu
12	167.5	18.3	348	2 T28623	hypothetical prote
13	165	18.1	335	2 A40036	apoptosis-mediati
14	153	16.8	314	2 I37383	FAS soluble protei
15	151	16.5	250	1 A49053	CD27 antigen precu
16	145	15.9	271	2 S12783	OX40 antigen precu
17	142	15.6	272	2 I48700	gene OX40 protein
18	135.5	14.8	277	2 I37552	OX40 homolog - hum
19	130	14.2	416	1 JN0006	nerve growth facto
20	129.5	14.2	461	1 GQRT11	tumor necrosis fac
21	129	14.1	326	1 GOVZML	T2 protein - myxom
22	128.5	14.1	454	1 GQXST1	tumor necrosis fac
23	125.5	13.7	455	1 GQHTU1	tumor necrosis fac
24	121	13.3	651	2 JC7705	death receptor-6 -
25	116	12.7	325	2 B43692	T2 protein - rabbi
26	115.5	12.7	427	1 GQHUN	nerve growth facto
27	111	12.2	1069	2 T42681	hypothetical prote
28	109.5	12.0	461	2 JC4302	tumor necrosis fac
29	109.5	12.0	1274	2 T42017	cysteine rich prot

30 108.5 11.9 425 1 A26431  
31 108 11.8 22 2 B60771  
32 107 11.7 832 2 A31246  
33 107 11.7 833 2 S19087  
34 107 11.7 890 2 S00670  
35 107 11.7 1790 1 MMFBL1  
36 106 11.6 2406 2 A54148  
37 106 11.6 2515 2 S47008  
38 105 11.5 937 2 I53282  
39 103.5 11.3 1548 2 S34583  
40 103.5 11.3 13288 2 T03099  
41 103 11.3 751 2 F87789  
42 103 11.3 810 2 T10756  
43 101 11.1 932 2 I52527  
44 100.5 11.0 686 2 JC7569  
45 100 11.0 685 2 JC7570

#### ALIGNMENTS

##### RESULT 1

A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C>Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.//  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:9356608; PMID:2475341  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:Cross-references: EMBL:X60592; NID:g29850; PID:CAA43045.1; PID:g29851  
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A:Reference number: A60771; MUID:89093941; PMID:2463309  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics:  
A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CYT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 86.0%; Score 785; DB 2; Length 277;

Best Local Similarity 95.1%; Pred. No. 5.8e-57;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLMGCLLTAVHPPTACREKQVLYNSQCCSLCQPKQLVSDCTETETECFL 60  
DB 1 MVRPLQCVLMGCLLTAVHPPTACREKQVLYNSQCCSLCQPKQLVSDCTETETECFL 60  
QY 61 PCGSEFLDWNRTTHCHQKVCNPLGLRVQKGTSETDTICTCEGWHCTSEACSECV 120  
DB 61 PCGSEFLDWNRTTHCHQKVCNPLGLRVQKGTSETDTICTCEGWHCTSEACSECV 120  
QY 121 LHRSCSPGFQKQIAVRPKTWLC 143  
DB 121 LHRSCSPGFQKQIAVRPKTWLC 143

## RESULT 2

A46476  
 B cell-associated surface molecule CD40, long splice form - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
 C:Accession: A46476; A46515  
 R:Torres, R.M.; Clark, E.A.  
 J. Immunol. 146, 620-626, 1992  
 A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine A:Reference number: A46476; MUID:92105763; PMID:1370315  
 A:Accession: A46476  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-305 <TOR>  
 A:Cross-references: GB:M83312; NID:g1553058  
 A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)  
 A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0.  
 R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992  
 A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
 A:Reference number: A46515; MUID:93094586; PMID:1261194  
 A:Accession: A46515  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-287, 'LV' <GRI>  
 A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N: A:Experimental source: BALB/c, liver  
 A:Note: sequence extracted from NCBI backbone (NCBI:P:120357)  
 C:Comment: For an alternative splice form, see PIR:A46515.  
 C:Comment: For an alternative splice form, see PIR:A46476.  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology  
 C:Keywords: alternative splicing; transmembrane protein  
 F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 52.98; Score 483; DB 2; Length 305;  
 Best Local Similarity 54.98; Pred. No. 2.4e-32;  
 Matches 79; Conservative 21; Mismatches 44; Indels 0; Gaps 0;

Qy 1 MVRPLQCVLWGLLTAVHPPEPTACRQYKYLINSQCCLCPQKQLVSDCTEFTTECL 60  
 Db 1 MVSPLRLCALWGLLTAVHLGQCVCSDKQYLDHGGCCDLCPGSLTSHCTALEXTQCH 60  
 Qy 61 PCGSEFLDWNRETHCHQYKCDPNGLRVQKQTSFTTICTCBEGHCHTSEACSCV 120  
 Db 61 PCDSGEFSQAWNREIRCHQHRHCEPNGLRVKKEGTAEISTVCTCKEGQCHTCKDCEACA 120  
 Qy 121 LHRSCSPGPGVKQIAVRPK\*WLCN 144  
 Db 121 QHTPCIEFGVGMENATTTTIVCH 144

## RESULT 3

A35356  
 tumor necrosis factor receptor 2 precursor [validated] - human  
 N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
 C:Species: Homo sapiens (man)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 27-Oct-2003  
 C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
 R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
 Science 248, 1019-1023, 1990  
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A:Reference number: A35356; MUID:90260639; PMID:2160731  
 A:Accession: A35356  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <SMI>  
 A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A:Reference number: A36475; MUID:91045991; PMID:2172983  
 A:Accession: A36475

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-195, 'R', 197-461 <KOH>  
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
 R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Cytokine 2, 231-237, 1990  
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690; PMID:1966549  
 A:Accession: A48416  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 23-461 <DEM>  
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
 A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)  
 R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat A:Reference number: A36007; MUID:90349572; PMID:2166946  
 A:Accession: A36007  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
 A:Cross-references: GB:M55957; NID:g339751; PIDN:AAA63262.1; PID:g339752  
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
 J. Biol. Chem. 265, 20131-20138, 1990  
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec A:Reference number: A23666; MUID:91056048; PMID:2173696  
 A:Accession: A23666  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 23-40; 65-89; 136-141; 300-306 <LOE>  
 R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f A:Reference number: A35010; MUID:90110215; PMID:2153136  
 A:Accession: B35010  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 27-31 <ENG>  
 R:Kuhnert, P.; Kemper, O.; Wallach, D.  
 Gene 150, 381-386, 1994  
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of A:Reference number: I38094; MUID:95121934; PMID:7821811  
 A:Accession: I38094  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-37 <RES>  
 A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:g825701  
 C:Genetics:  
 A:Gene: GDB:TNER2  
 A:Cross-references: GDB:125914; OMIM:191191  
 A:Map position: 1p36.2-1p36.2  
 A:Introns: 26/3  
 A:Note: the list of introns is incomplete  
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
 F:40-76/Domain: NGF receptor repeat homology <NG1>  
 F:78-119/Domain: NGF receptor repeat homology <NG2>  
 F:120-162/Domain: NGF receptor repeat homology <NG3>  
 F:164-201/Domain: NGF receptor repeat homology <NG4>  
 F:262-279/Domain: transmembrane #status predicted <TMN>  
 F:280-461/Domain: intracellular #status predicted <INT>  
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.3%; Score 212.5; DB 1; Length 461;  
 Best Local Similarity 34.5%; Pred. No. 3.6e-10;  
 Matches 51; Conservative 12; Mismatches 58; Indels 27; Gaps 6;

Qy 4 LPQLCVLWGLLTAVHPPEPTACRQYKYLINS--QCCLCPQKQLVSDCTEFTTECLP 61  
 Db 23 LPAQVA-----FTPAPEFGSTRLREYDQTAMCCSKCSPGQHAQVCTIKTSDTVCD 77

QY 62 CCESEFLDWNRETHCHQHKYCDPNLGLRVQ-----QKGTSETDTTCTCEEGWHCT--- 112  
 Db 78 CEDSTYTQLMNVPEC-----LSCGSRCSDDQVETQACTREQNRICTRCPGMYCALSK 130

QY 113 SEACESCVLHRS CSPGFGVKQIAVRPKT 140  
 Db 131 QEGRLCAPLRKCRPGFGV-----ARPGT 154

RESULT 4  
 154182  
 tumor necrosis factor receptor 2-related protein - human  
 C:Species: Homo sapiens (man)  
 C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
 C:Accession: I54182  
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
 Genomics 16, 214-218, 1993  
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen  
 A:Reference number: I54182; MUID:93252381; PMID:8486360  
 A:Accession: I54182  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-435 <RES>  
 A:Cross-references: GB:L04270; NID:g3339761; PIDN:AAA36757.1; PID:g3339762  
 C:Gene: GDB:LTBR  
 A:Cross-references: GDB:1230195; OMIM:600979  
 A:Map position: 12p13.3-12p13.1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 21.9%; Score 200; DB 2; Length 435;  
 Best Local Similarity 36.5%; Pred. No. 3.6e-09;  
 Matches 50; Conservative 15; Mismatches 58; Indels 14; Gaps 6;

QY 5 PLQCVLWGLTAVHPE--PPTA-----CR--EKQYLINSQ--CCSLQCPQKLVSDCTE 53  
 Db 16 PLVLGLFG-LLAASQPAVPPYASENQTCDQEKYVFPQHRICGSRCPGTYVSAKCSR 74

QY 54 FTEITCLCGSEFLDWNRETHCHQHKYCDPNLGLRVQKGTSETDTTCTCEEGWHCTS 113  
 Db 75 IRDTVCATCAENSNEHWNLYTICQLCRPCDPFWGLBETAPCTSKRTKTCRCQCPGMCAA 134

QY 114 EA--CESCVLHRS CSPG 128  
 Db 135 WALECTHCELLSDCCPG 151

RESULT 5  
 JC2395  
 Fas antigen precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Jul-2003  
 C:Accession: JC2395; PC2246  
 R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
 Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
 A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat live  
 A:Reference number: JC2395; MUID:94128114; PMID:7507668  
 A:Accession: JC2395  
 A:Molecule type: mRNA  
 A:Residues: 1-324 <KIM>  
 A:Cross-references: DBJ:D26112; NID:G468486; PIDN:BAA05108.1; PID:d1005650; PID:g468487  
 A:Experimental source: thymus  
 A:Accession: PC2246  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 'RPT', <K12>  
 A:Cross-references: DBJ:D26113; NID:G468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489  
 A:Experimental source: liver  
 C:Genetics:  
 C:Introns: 62/1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-324/Product: Fas antigen #status predicted <NAT>  
 F:44-79/Domain: NGF receptor repeat homology <NGF>  
 F:81-124/Domain: NGF receptor repeat homology <NG4>  
 F:171-188/Domain: transmembrane #status predicted <TM>

Query Match 20.6%; Score 188.5; DB 2; Length 324;  
 Best Local Similarity 30.6%; Pred. No. 2.4e-08;  
 Matches 44; Conservative 20; Mismatches 69; Indels 11; Gaps 5;

QY 21 EPPTACREKQYLINSQCCLCPQKLVSDC-TEFTETECPLCGE-SEFLDTWNRETHCH 78  
 Db 39 ETDNNGCEGLYQVGFPCQCPQGERKVKDCTTGGAPTCHPCTEGEYVTDKRYSDKCR 98

QY 79 OHKQCDPNLGLRVQKGTSETDTTCTCEEGWHCTSEACSCVLHRS CSPGFGVKQI---A 135  
 Db 99 RCACFDCEHGLEVETNCTRTQNTCKCKENFYCNASLCHDCHYCTSC-----GLIEDILEPC 154

QY 136 VRPKTWLCNRQAQT--RLMLSVVP 157  
 Db 155 TRTSNTKCKKQSSNYKLLWLLIIP 178

RESULT 6  
 A46484  
 apoptosis-mediating membrane-associated polypeptide Fas - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Jul-2003  
 C:Accession: A46484; A47254  
 R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J.; Immunol. 148, 1274-1279, 1992  
 A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas anti  
 A:Reference number: A46484; MUID:92148151; PMID:1371136  
 A:Accession: A46484  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-327 <NAT>  
 A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
 A:Experimental source: BAM3 macrophage cell line  
 A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
 R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
 A:Title: Aberrant transcription caused by the insertion of an early transposable element  
 A:Reference number: A47254; MUID:93189576; PMID:7680478  
 A:Accession: A47254  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-96 <ADA>  
 A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506  
 A:Experimental source: MRL lpr/lpr  
 A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863,  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: transmembrane protein  
 F:44-79/Domain: NGF receptor repeat homology <NGF>  
 F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 19.7%; Score 180; DB 2; Length 327;  
 Best Local Similarity 33.6%; Pred. No. 1.2e-07;  
 Matches 49; Conservative 15; Mismatches 68; Indels 14; Gaps 6;

QY 18 VHPPTACREKQYLINSQCCLCPQKLVSDCTEFTET-ECPLCGE-SEFLDTWNRET 75  
 Db 37 VH-ETDNKNCSEGLYQVGFPCQCPQGERKVKDCTTGGAPTCHPCTEGEYVTDKRYSDKCR 95

QY 76 HCHQHKYCDPNLGLRVQKGTSETDTTCTCEEGWHCTSEACSCVLHRS CSPGFGVKQIA 135  
 Db 96 KCRRTCLCDEHGLEVETNCTRTQNTCKCKPDPFYCDSPGCGEHCVCASCEHG-----T 149

QY 136 VRPKTWL-----CNRQA--OTRMLSVV 156  
 Db 150 LEPCTATNTNCRKQSPNRNLWLLTI 175

RESULT 7

148854  
 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 27-Oct-2003  
 C:Accession: U48854  
 R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
 Mamm. Genome 5, 726-727, 1994  
 A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
 A:Reference number: 148854; MUID:95176849; PMID:7873884  
 A:Accession: U48854  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-459 <RES>  
 A:Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831  
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
 F:151-188/Domain: NGF receptor repeat homolog <NGF>

Query Match 19.1%; Score 174.5; DB 2; Length 459;  
 Best Local Similarity 29.9%; Pred. No. 4.4e-07;  
 Matches 41; Conservative 20; Mismatches 59; Indels 17; Gaps 6;

QY 4 LPLQCVLWGLLTAHVHPEPTACREKQYLIN---SQCSSLCPGQKLVSDCTFTETECIL 60  
 DB 8 VPAQV-----LTPKEPGVEYCOISQYDYDKAQMCCAKCPGQYVKHF 62  
 QY 61 PCGESEFLDTWNRTHCHQHYCDPNLGL-RVQOKG-TSETDTICTCEGWHCT-----SE 114  
 DB 63 DCEASMTQVWNPRTCLS---CSSSCTDQVETRACTKQNRVCAACEAGRYCALXTHSG 119  
 QY 115 ACESCVLHRSCTSPGFGV 131  
 DB 120 SCRCMELSKCGPGFGV 136

RESULT 8  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 27-Oct-2003  
 C:Accession: B38634; A40254; S54816  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
 A:Reference number: A38634; MUID:91187885; PMID:1849278  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEW>  
 A:Cross-references: GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828  
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
 A:Reference number: A40254; MUID:91246168; PMID:1645445  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GOO>  
 A:Cross-references: GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828  
 R:Kisssonerghis, M.; Fallowes, R.; Feldmann, M.; Chernajovsky, Y.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
 A:Reference number: S54816  
 A:Accession: S54816  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <KTS>  
 A:Cross-references: EMBL:X87128; NID:G809043; PIDN:CAA60618.1; PID:G809044  
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F:40-77/Domain: NGF receptor repeat homolog <NG1>  
 F:79-120/Domain: NGF receptor repeat homolog <NG2>  
 F:166-203/Domain: NGF receptor repeat homolog <NG4>

Query Match 18.9%; Score 173; DB 2; Length 474;  
 Best Local Similarity 28.6%; Pred. No. 6e-07;  
 Matches 42; Conservative 21; Mismatches 64; Indels 20; Gaps 6;

QY 2 VRLPQCVLWG-----CLLTAVHPEPTACREKQYLIN---SQCSSLCPGQKLVSD 50  
 DB 8 VALVPELQWATGHTVPAQVVLTPKPEPGVECOISQYDYDKAQMCCAKCPGQYVKHF 67  
 QY 51 CTEFTETETCLCGSESEFLDTWNRTHCHQHYCDPNLGL-RVQOKG-TSETDTICTCEG 108  
 DB 68 CNKTSDTVCADCEASMTQVWNPRTCLS---CSSSCTDQVETRACTKQNRVCAACEAG 124  
 QY 109 WHCT---SEACESCVLHRSCTSPGFGV 131  
 DB 125 RYCALXTHSGRCRCMELSKCGPGFGV 151

RESULT 9  
 D72175  
 G2R protein - variola minor virus (strain Garcia-1966)  
 C:Species: variola minor virus  
 C:Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 15-Sep-2003  
 C:Accession: D72175  
 R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Massung, R.F.; Lopare  
 submitted to GenBank, March 1998  
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor  
 A:Reference number: A72150  
 A:Accession: D72175  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-349 <SHC>  
 A:Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54798.1; PID:95830759  
 A:Experimental source: strain Garcia-1966  
 C:Genetics: G2R  
 C:Gene: G2R  
 C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homolog

Query Match 18.6%; Score 170; DB 2; Length 349;  
 Best Local Similarity 29.0%; Pred. No. 8.3e-07;  
 Matches 38; Conservative 21; Mismatches 64; Indels 8; Gaps 4;

QY 6 LQCVLWGLLTAHVHPEPTACREKQYLINQCSSLCPGQKLVSDCTFTETECILPGCES 65  
 DB 12 LSCIINGRDAAPTPPNGKCKDTEYKRNLCCLSCPCPGIYASRLCDKSKTNTCTPCGSG 71  
 QY 66 EFLDTWNRTHCHQ-HRYCDPNLGLRVQOKGTSET-DTICTCEGWHCT---SEACESCV 120  
 DB 72 TFTSRNNHLPACLSGRCNCNSN---QVETRSCTNTHNRCICSPGYICLLKSGSGCKACV 128  
 QY 121 LHRSCSPGFGV 131  
 DB 129 SQTKCGIGYGV 139

RESULT 10  
 D36858  
 gene G4R protein - variola virus  
 N:Alternate names: B28R protein (COP)  
 C:Species: variola virus  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Sep-2003  
 C:Accession: D36858; S46888; S32385; S35987  
 R:Blinov, V.M.  
 submitted to GenBank, November 1992  
 A:Reference number: A36859  
 A:Accession: D36858  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-349 <BLI>  
 A:Cross-references: GB:X69198; NID:9456758; PIDN:CAA49137.1; PID:94567087  
 A:Experimental source: strain India-1967, sep. major, isolate Ind3  
 R:Kolykhalov, A.A.; Blinov, V.M.; Gutorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolo  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P C

A:Reference number: S46868

A:Accession: S46888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <KOL>

A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449

A:Experimental source: strain India-1967, isolate Ind3

R:Shchelkunov, S.N.; Blinov, V.M.; Sandakchiev, L.S.

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A:Reference number: S32385; MUID:93202281; PMID:8384129

A:Accession: S32385

A:Molecule type: DNA

A:Residues: 31-168 <SHC>

A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major

C:Genetics:

A:Gene: G4R

C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A:Reference number: S32385; MUID:93202281; PMID:8384129

A:Accession: S32385

A:Molecule type: DNA

A:Residues: 31-168 <SHC>

A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major

C:Genetics:

A:Gene: G4R

C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A:Reference number: S32385; MUID:93202281; PMID:8384129

A:Accession: S32385

A:Molecule type: DNA

A:Residues: 31-168 <SHC>

A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major

C:Genetics:

A:Gene: G4R

C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A:Reference number: S32385; MUID:93202281; PMID:8384129

A:Accession: S32385

A:Molecule type: DNA

A:Residues: 31-168 <SHC>

A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major

C:Genetics:

A:Gene: G4R

C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A:Reference number: S32385; MUID:93202281; PMID:8384129

A:Accession: S32385

A:Molecule type: DNA

A:Residues: 31-168 <SHC>

A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major

C:Genetics:

A:Gene: G4R

C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

C:Keywords: duplication; glycoprotein; homodimer; phosphoprotein; receptor; surface anti

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-260/Product: CD27 antigen #status predicted <MAT>

F:21-191/Domain: extracellular #status predicted <EXT>

F:27-63/Domain: NGF receptor repeat homology <NG1>

F:65-105/Domain: NGF receptor repeat homology <NG2>

F:121-188/Region: proline/serine/threonine-rich

F:192-211/Domain: transmembrane #status predicted <TMN>

F:212-260/Domain: intracellular #status predicted <INT>

F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.3%; Score 167.5; DB 1; Length 260;

Best Local Similarity 34.5%; Pred. No. 1.1e-06;

Matches 40; Conservative 15; Mismatches 52; Indels 9; Gaps 7;

QY 8 CVLWGCLLTAVHPEPTACREKQVLYNSQ-CCSLCOPGQKLVSDCTEFTET-ECLPC--G 63

Db 10 CVL-GTLVGLSATPAPKSCPERHYWAQKLCQCCQCEGTELVKDCDQHRXTAQCDPIGP 68

QY 64 ESEFLDTWNRETHQHKYCDPNLGLRVQKQKGTSET-DTICTCEEGWHCT---SEACEGCV 119

Db 69 VS-FSPDHTPHCESCRHC--NSGLLV-RNCTITANAECACRNGWQCRDKECTEC 120

RESULT 12

T28623

C:Species: variola major virus

C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 15-Sep-2003

C:Accession: T28623

R:Masung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin,

Nature 366, 748-751, 1993

A:Title: Potential virulence determinants in terminal regions of variola smallpox virus

A:Reference number: 220488; MUID:94088747; PMID:8264798

A:Accession: T28623

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-348 <MAS>

A:Cross-references: EMBL:I22579; NID:G623595; PIDN:AAA60933.1; PID:G439102

A:Experimental source: strain Bangladesh 1975

C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 18.3%; Score 167.5; DB 2; Length 348;

Best Local Similarity 29.8%; Pred. No. 1.3e-06;

Matches 39; Conservative 21; Mismatches 62; Indels 9; Gaps 5;

QY 6 LQCVLWGCLLTAVHPEPTACREKQVLYNSQCCSLCOPGQKLVSDCTEFTET-ECLPCGES 65

Db 12 LSCIINGRDAAPYTPNGKCKDTEYKRNLCCLSCPPGTAYASRLCDSKNTQCTPCGSG 70

QY 66 EFLDTWNRETHQHKYCDPNLGLRVQKQKGTSET-DTICTCEEGWHCT---SEACEGCV 120

Db 71 TFTSRNHLPACLSCNGRCNSN---QVETRSCNTHNRICECSPGYVCLLKSGSGCKACV 127

QY 121 LHRSCSPGFGV 131

Db 128 SQTCKGIGYGV 138

RESULT 13

A40036

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi

A:Reference number: A40036; MUID:91309137; PMID:1713127

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Cross-references: GDB:132582; OMIM:186711

A:Map position: 12p13-12p13

A:Introns: 46/1; 90/1; 150/1; 180/1; 220/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi

A:Reference number: A40036; MUID:91309137; PMID:1713127

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Cross-references: GDB:132582; OMIM:186711

A:Map position: 12p13-12p13

A:Introns: 46/1; 90/1; 150/1; 180/1; 220/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi

A:Reference number: A40036; MUID:91309137; PMID:1713127

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Cross-references: GDB:132582; OMIM:186711

A:Map position: 12p13-12p13

A:Introns: 46/1; 90/1; 150/1; 180/1; 220/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi

A:Reference number: A40036; MUID:91309137; PMID:1713127

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <ITO>  
A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410  
R:Krammer, P.H.  
Submitted to the EMBL Data Library, February 1992  
A:Reference number: S24543  
A:Accession: S24543  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-335 <KRA>  
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742  
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich  
J. Biol. Chem. 267, 10709-10715, 1992  
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member  
A:Accession number: A38142; MUID:92268122; PMID:1375228  
A:Accession: A38142  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-134, 'Q', 136-335 <OE>  
A:Experimental source: SKW6.4 cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)  
A:Note: in NCBI backbone the source is designated as mouse  
C:Genetics:  
A:Gene: GDB:AP71  
A:Cross-references: GDB:132671; OMIM:134637  
A:Map position: 10q24.1-10q24.1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: apoptosis; surface antigen; transmembrane protein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:185-128/Domain: NGF receptor repeat homology <NG4>  
F:174-190/Domain: transmembrane #status predicted <TMN>  
Query Match 18.1%; Score 165; DB 2; Length 335;  
Best Local Similarity 29.2%; Pred. No. 2e-06; Indels 22; Gaps 5;  
Matches 40; Conservative 18; Mismatches 57  
QY 37 CCSLCQPGKLVSDCT-EFTETCLPCGE-SFELDTWNRTHCHQHKYCDPNLGLRVQOK 94  
DB 59 CHKPCPPGERKARDCTVNGDEPDVCPQEGKEYTDKAHFSSKRCRLCDEGHGLEVEIN 118  
QY 95 GTSETDTICTCEGWHCTSEACSVLHRSCTSPGFGVKQIAVRPKT-----WL 142  
DB 119 CTRTQNTKCRCKPNFNSVCEHCDPCTKCEHGI-IKECTLTNT-KCKEVEK 177  
QY 143 CNRQATQLMLSVVPI 159  
DB 178 C-----LALLPIPLI 187  
RESULT 14  
137383  
FAS soluble protein - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 07-Jul-2003  
C:Accession: I37383  
R:Cascino, I.; Ficuci, G.; Papoff, G.; Ruberti, G.  
J. Immunol. 154, 2706-2713, 1995  
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are  
A:Reference number: I37383; MUID:95181785; PMID:7533181  
A:Accession: I37383  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-314 <RES>  
A:Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA8031.1; PID:g695539  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
Query Match 16.8%; Score 153; DB 2; Length 314;  
Best Local Similarity 29.3%; Pred. No. 1.8e-05;  
Matches 34; Conservative 19; Mismatches 59; Indels 4; Gaps 4;  
QY 37 CCSLCQPGKLVSDCT-EFTETCLPCGE-SFELDTWNRTHCHQHKYCDPNLGLRVQOK 94  
DB 59 CHKPCPPGERKARDCTVNGDEPDVCPQEGKEYTDKAHFSSKRCRLCDEGHGLEVEIN 118

QY 95 GTSETDTICTCEGWHCTSEACSVLHRSCTSPGFGVKQIAVRPKTLCNRAQTR 150  
DB 119 CTRTQNTKCRCKPNFNSVCEHCDPCTKCEHGI-IKECTLTNT-KCKEVEK 172  
RESULT 15  
A49053  
CD27 antigen precursor - mouse  
N:Alternate names: CD27L receptor; T cell activation antigen CD27  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Dec-1993 #sequence\_revision 22-Apr-1995 #text\_change 11-Sep-1998  
C:Accession: A49053  
R:Graveststein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp, I.  
Eur. J. Immunol. 23, 943-950, 1993  
A:Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte  
A:Reference number: A49053; MUID:93209296; PMID:8384562  
A:Accession: A49053  
A:Molecule type: mRNA  
A:Residues: 1-250 <GRA>  
A:Note: sequence extracted from NCBI backbone (NCBIN:128169, NCBIP:128169)  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; trar  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-250/Product: CD27 antigen #status predicted <MAT>  
F:21-182/Domain: extracellular #status predicted <EXT>  
F:27-63/Domain: NGF receptor repeat homology <NGL>  
F:65-105/Domain: NGF receptor repeat homology <NG2>  
F:121-179/Region: proline/serine/threonine-rich  
F:183-202/Domain: transmembrane #status predicted <TMN>  
F:203-250/Domain: intracellular #status predicted <INT>  
F:95,162/Binding site: carbohydrate (asn) #status predicted  
Query Match 16.5%; Score 151; DB 1; Length 250;  
Best Local Similarity 28.2%; Pred. No. 2.2e-05;  
Matches 33; Conservative 18; Mismatches 54; Indels 12; Gaps 6;  
QY 11 WGLLTAV-----HPRPTACREKQVLI-NSCCSLCQPGKLVSDC-TEFTETCLPC-- 62  
DB 8 WLCMLGTLVGLSATLAFNSCPDKHYWTGGGLCCRMCEGTFVVKDCQDRFAAQDCIP 67  
QY 63 GESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGSETDTICTCEGWHCTSEACESC 119  
DB 68 GTS-PSPDYHTRPHCESCRHCNSGLIR---NCTVTANAEGCSKNWQCRDQECTEC 120  
Search completed: July 21, 2004, 10:07:17  
Job time : 17 secs